SEQUENCE LISTING

SEQ ID NO: 1 BLM gene cluster ORFS 30 through 8

(note orf 31-40 on sequence 1-18660 are translated on the reverse strand and on a separate file)

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18601  ACCCATCTCATAGGTGTACGCGCTGGAGCATTCGGGGCACGACGGAAGGTTCTCGGTCAC   18660

18661  GAGAGCACTGTAAGCCCGAACCCGCAAGGATGACGAATTGCAAAATTGTGCAAGTCGCTA   18720

18721  CATGATGGTCCGGCTGTGCCCGCAGGTAGCCGCGGGCACAGCACCAGACGCTGCCTCCGC   18780

18781  GCACCGCGCGGGAGGCCCGGTGAGGCGAGAGGCTGAGGTTCCGTGCCGGTTCCGCTGTAT   18840
                                                M  P  V  P  L  Y    (orf30)

18841  CAGGCGAAGGCCGAGTTCTTCCGGATGCTGGGGCACCCGGTCCGCATCCGCGTACTGGAG   18900
       Q  A  K  A  E  F  F  R  M  L  G  H  P  V  R  I  R  V  L  E

18901  CTGCTGCAGGACGGGCCGATGCCGGTGCGTGATCTGCTGGCGGCGATCGAGATCGAGCCC   18960
       L  L  Q  D  G  P  M  P  V  R  D  L  L  A  A  I  E  I  E  P

18961  TCGGCGCTGTCCCAGCAGCTGGCGGTGTTGCGCCGCTCGGGCATCGTGACCTCCACCCGC   19020
       S  A  L  S  Q  Q  L  A  V  L  R  R  S  G  I  V  T  S  T  R

19021  ACGGGTTCCACGGTCGTCTACGAGCTGGCCGGTGGCGACGTGGCGGAGCTGATGTCCGCC   19080
       T  G  S  T  V  V  Y  E  L  A  G  G  D  V  A  E  L  M  S  A

19081  GCGCGCCGCATCCTGACCGAGATGCTCAATGGGCAGCACGAGCTGCTGGAGGAGCTGAGG   19140
       A  R  R  I  L  T  E  M  L  N  G  Q  H  E  L  L  E  E  L  R

19141  GAAGCCGAGGTCAGTGCCCGGTGAGCTCCCTCGCCGTCCGGGTGGGAGCCCGGGTGCGTT   19200
       E  A  E  V  S  A  R  *
                              M  S  S  L  A  V  R  V  G  A  R  V  R  S   (orf29)

19201  CCGTGCTGCCCACCCGCGCCGACCTCGCGGGCATGGGCCGCAGCCCGCGACGTGATCTAC   19260
         V  L  P  T  R  A  D  L  A  G  M  G  R  S  P  R  R  D  L  L

19261  TGGCCGGTCTGACCGTGGCGATCGTGGCCCTGCCGCTCGCCCTCGGATTCGGCGTCTCCT   19320
         A  G  L  T  V  A  I  V  A  L  P  L  A  L  G  F  G  V  S  S

19321  CCGGTCTCGGCGCGGAGGCAGGGCTGGCCACCGCGGTGGTGGCGGGCGCGCTGGCCGCGG   19380
         G  L  G  A  E  A  G  L  A  T  A  V  V  A  G  A  L  A  A  V

19381  TATTCGGTGGGTCGAATCTCCAGGTGTCCGGGCCCACGGGCGCCATGACCGTGGTCCTGG   19440
         F  G  G  S  N  L  Q  V  S  G  P  T  G  A  M  T  V  V  L  V

19441  TGCCCATCGTCGCCCGGTACGGCCCCGGCGGTGTCCTCACGGTCGGCCTGCTCGCCGGAC   19500
         P  I  V  A  R  Y  G  P  G  G  V  L  T  V  G  L  L  A  G  L

19501  TGATGCTGATCGCGCTCGCCCTCGCCCGCGCCGGCCGCTACATGCAGTACGTGCCGGCCC   19560
         M  L  I  A  L  A  L  A  R  A  G  R  Y  M  Q  Y  V  P  A  P

19561  CGGTGGTGGAGGGCTTCACCCTCGGCATCGCCTGCGTGATCGGCTTGCAGCAGGTGCCGA   19620
         V  V  E  G  F  T  L  G  I  A  C  V  I  G  L  Q  Q  V  P  N

19621  ACGCCCTGGGAGTCGCCAAGCCGGAGGGCGACAAGGTCCTCGTCGTGACCTGGCGCGCGG   19680
         A  L  G  V  A  K  P  E  G  D  K  V  L  V  V  T  W  R  A  V

19681  TCGAGACCTTCGCCGGGGCGCCCAACTGGACCGCTGCCGGACTGGCGGCAGCGGTCGCCG   19740
         E  T  F  A  G  A  P  N  W  T  A  A  G  L  A  A  A  V  A  A

19741  CGGTCATGCTGACCGGCGCGCGGTGGCGGCCGGTCGTTCCCTTCTCCCTCCTCGCGGTGA   19800
         V  M  L  T  G  A  R  W  R  P  V  V  P  F  S  L  L  A  V  T

19801  CCGGTGCCACCGTCGTGGCCCAGCTGTGCCACCTGGACGCGGCCCGCCCGATCGGGGACC   19860
         G  A  T  V  V  A  Q  L  C  H  L  D  A  A  R  P  I  G  D  L

19861  TGCCCGCGGGGCTGCCCGCCCCGTCGCTGGCCTTCCTGGACCTCGGAGCACTGGGCTCGC   19920
         P  A  G  L  P  A  P  S  L  A  F  L  D  L  G  A  L  G  S  L

19921  TGCTGGCGCCTGCCGTGGCCGTGGCGGCCCTTGCCGCGTTGGAATCGCTGCTGTCGGCGT   19980
         L  A  P  A  V  A  V  A  A  L  A  A  L  E  S  L  L  S  A  S
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19981  CCGTCGCGGACGGCATGACGGTCGGGCAGAAGCACGACCCGGACAAGGAGCTGTTCGGGC  20040
         V  A  D  G  M  T  V  G  Q  K  H  D  P  D  K  E  L  F  G  Q

20041  AGGGTCTCGCCAACCTGGCCGCCCCGCTGTTCGGCGGCGTCCCGGCCACCGGCGCGATAG  20100
         G  L  A  N  L  A  A  P  L  F  G  G  V  P  A  T  G  A  I  A

20101  CCCGCACCGCCGTCAACGTCCGTACCGGTGCGAGCTCGCGACTGGCGGCCCTCACGCACG  20160
         R  T  A  V  N  V  R  T  G  A  S  S  R  L  A  A  L  T  H  A

20161  CCGCGATCCTCGCCGTCATCGTCTTCGCCGCCGCCCCACTGGTCTCCCGCATCCCCCTGG  20220
         A  I  L  A  V  I  V  F  A  A  A  P  L  V  S  R  I  P  L  A

20221  CCGCGCTCGCCGGCGTGCTGATCGCGACCGCGATCCGCATGGTCGAAGTGGGCAGCCTGC  20280
         A  L  A  G  V  L  I  A  T  A  I  R  M  V  E  V  G  S  L  R

20281  GGGCGATGGCCCGCGCCACGCGCTCCGACGGCCTGGTACTGATCCTCACGGCGGTCGCCA  20340
         A  M  A  R  A  T  R  S  D  G  L  V  L  I  L  T  A  V  A  T

20341  CCGTGGCCCTGGACCTCGTCTACGCCGTCATCATCGGCCTGCTGGTCGCCGGCGCACTCG  20400
         V  A  L  D  L  V  Y  A  V  I  I  G  L  L  V  A  G  A  L  A

20401  CCCTGCGGGCCGTGGCCAAGCAGGTCCGCCTGGACCAGGTCTCCTTGAAGGAGGACCTGA  20460
         L  R  A  V  A  K  Q  V  R  L  D  Q  V  S  L  K  E  D  L  T

20461  CCGGCGACCACAGCGCCGAGGAACACGCGCTGCTCGCCGAGCACATCGTGGCGTACCGCA  20520
         G  D  H  S  A  E  E  H  A  L  L  A  E  H  I  V  A  Y  R  I

20521  TCGACGGTCCGCTGTTCTTCGCCGCGGCCCACCGCTTCCTGCTGGAACTCTCGGACGTCG  20580
         D  G  P  L  F  F  A  A  A  H  R  F  L  L  E  L  S  D  V  A

20581  CGGACGTGCGCGTGGTGATCCTGCGCATGTCCCGCGTGACCACCATGGACGCCACCGGCG  20640
         D  V  R  V  V  I  L  R  M  S  R  V  T  T  M  D  A  T  G  A

20641  CCCTCGTCCTGAAGGACGCGGTCACCAAGCTGAACCGGCGCGGCATCACCGTCCTGGCCT  20700
         L  V  L  K  D  A  V  T  K  L  N  R  R  G  I  T  V  L  A  S

20701  CCGGGGTACGCCCCGGCCAGCGCCGGGTCCTCGACTCCGTCGGCGCCCTCGGTCTGCTCC  20760
         G  V  R  P  G  Q  R  R  V  L  D  S  V  G  A  L  G  L  L  R

20761  GGGCCGCCACCGGCGACGACTACACCGGCACTCCCGAAGCCATCGCCGCCGCCCGAAGCC  20820
         A  A  T  G  D  D  Y  T  G  T  P  E  A  I  A  A  A  R  S  H

20821  ACCTGCACGGCGCCGGTGTCCTGGCCCCCGCCTGCCCGGGCCCGCCTCCTCCGGTACCCC  20880
         L  H  G  A  G  V  L  A  P  A  C  P  G  P  P  P  P  V  P  P

20881  CACCGTGCGCTCCGAGTGCCCGACGATGAGGAGCCGACCGAGGTCCTCCTCCGTCACCCG  20940
         P  C  A  P  S  A  R  R  *

20941  GACACCCACGGTTGCGCCGCCCCATGCCGGCGGTCCCTCCTGACGGCCCGTCCGCGGCTT  21000

21001  GAGGCGGCGGTGGACGGCCTGCCGCCGCCGGCCTCGGGCTGATCGGCGTGATCACCGCCC  21060

21061  ATGCGCGGGTGGGCGCCCGCGGCATCGTGGGCGGGACCGTGTTCCCGGCCACCGCGGCGG  21120

21121  CCGGCCTCGCGCTGGGCGTGGCCTGCCGCGGTGCCTGGTAGCGGCGGGGTCCGGCGGCCG  21180

21181  GGCCTGTGCTTCTTCCCGCCCGTCCGGCGGGTGGCGCCGCGCCGGCGGTGACAGGGAAAT  21240

21241  ATGACCGGAACTGGGATGCTCGCGTCCACTCGGGTGTGTTTAAGTGCCACGGGGGCTTCC  21300

21301  GACGGCGCGTCGCGCGCCGGCGGTTCGCCCGATGATGGTCGTGCGGCGCTGTGAGCCGGG  21360

21361  GAGCCTATGGCACAGGACCTGAACGACTGGATCGAGGACGAGGTCGTCCCTTACGAGGAG  21420
              M  A  Q  D  L  N  D  W  I  E  D  E  V  V  P  Y  E  E     (orf28)

21421  AAGCCTCTCGAATGGATCTCCCAGTACCACTTCTTCCGCGACCCGGCGCGAGCCGCCTAT  21480
         K  P  L  E  W  I  S  Q  Y  H  F  F  R  D  P  A  R  A  A  Y

21481  GTCGATCACACCTACTTCTTCTCACCGGCCGATGGCGCGATCGTCTACCAGAAAGTAGTG  21540
         V  D  H  T  Y  F  F  S  P  A  D  G  A  I  V  Y  Q  K  V  V

21541  GATCCCCAGGAGTCGATCATCGACATCAAGGGGAAGCCGTACTCGCTGGCCGCCGCGCTC  21600
         D  P  Q  E  S  I  I  D  I  K  G  K  P  Y  S  L  A  A  A  L
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21601  CGTGACGAATCGTTCGGTCACCGGTGCCTGGTGATCGGCATCTTCATGACCTTCTTCGAC  21660
       R  D  E  S  F  G  H  R  C  L  V  I  G  I  F  M  T  F  F  D

21661  GTGCACATCAACCGGATGCCTTACGGCGGCCGTCTCTCCTTCGCGCTCAAGGAGCCCATC  21720
       V  H  I  N  R  M  P  Y  G  G  R  L  S  F  A  L  K  E  P  I

21721  GGGACGTTCAACCTCCCCATGCTGGCCATGGAGCAGGACCTGCTCGAACGGCTCCGGGTC  21780
       G  T  F  N  L  P  M  L  A  M  E  Q  D  L  L  E  R  L  R  V

21781  AATCCGGCTCACGCGAGGTATCTGCACCTGAACGAGCGGATGGTCAACCGGGTCGACGCG  21840
       N  P  A  H  A  R  Y  L  H  L  N  E  R  M  V  N  R  V  D  A

21841  CCGCGGCTCCGGGGCCCGTACTGGATGCTCCAGATCGCCGACTACGACGTCGACTCCATC  21900
       P  R  L  R  G  P  Y  W  M  L  Q  I  A  D  Y  D  V  D  S  I

21901  ACCCCGTTCTGCAGACGGCAGGGAATGTTCCGCTCCCAGGGGCGCCGCTTCTCCCAGATC  21960
       T  P  F  C  R  R  Q  G  M  F  R  S  Q  G  R  R  F  S  Q  I

21961  CGCTACGGATCGCAGGTCGACCTGGTGATCCCGATGGCGGCCGACCGCGAGTACGTCCCC  22020
       R  Y  G  S  Q  V  D  L  V  I  P  M  A  A  D  R  E  Y  V  P

22021  GTGGAGGCCGTCGGCCGGCACGTGAAGGCGGGGCTCGACCCGCTCGTCAAGATCCGGTGG  22080
       V  E  A  V  G  R  H  V  K  A  G  L  D  P  L  V  K  I  R  W

22081  CGTTGAAGAGCGCGTACGAAGCGATGGCGAACTGGAGGGACACAGCGTGGGTTTCCGTCG  22140
       R  *                                          M  G  F  R  R   (orf27)

22141  AGCGCAGAGGGCCGGTGGGCCGGGAGCGGGCCGGCGGGAGAGCGCCCGGTTCAGGCCGGA  22200
        A  Q  R  A  G  G  P  G  A  G  R  R  E  S  A  R  F  R  P  D

22201  CGGGCCGTCGGCGCCGCGGGACCGTCCGTTACCCCTGTCCGCCGGGCAGTTGTTCGAGTG  22260
        G  P  S  A  P  R  D  R  P  L  P  L  S  A  G  Q  L  F  E  W

22261  GGTGTTTGACAAGCTCGTCGACGGAGATCTGAGCCACCAGCCGACGATTGTGCGGCTCCG  22320
        V  F  D  K  L  V  D  G  D  L  S  H  Q  P  T  I  V  R  L  R

22321  CGGCCCGCTGAACACCGCCGCCCTGCGGATGGCCTACGCCCGGCTGGTGCGGCGCCACGA  22380
        G  P  L  N  T  A  A  L  R  M  A  Y  A  R  L  V  R  R  H  E

22381  GTGCCTGCGCACCCGCTTCCCCGTGATCGACGGGGAGCCCGTGCAGGTGATCGAGGGCAT  22440
        C  L  R  T  R  F  P  V  I  D  G  E  P  V  Q  V  I  E  G  I

22441  CGGGAAAGCAGCGGGGGGCCCGCTGCCGCTCATCGATCTGCGCCACCTCCCGGAGGCGCT  22500
        G  K  A  A  G  G  P  L  P  L  I  D  L  R  H  L  P  E  A  L

22501  TCGCGCGCGCGAGATCGCGAGGATCCGCGAGGAGACGCTGTCCACGCCGGTCCCCTTCGA  22560
        R  A  R  E  I  A  R  I  R  E  E  T  L  S  T  P  V  P  F  D

22561  CAAGCGGCCGCCCGTCCGCGTGGCGCTGATCCGGGCGGCGCCCGAGGAGCACCTCTTCCT  22620
        K  R  P  P  V  R  V  A  L  I  R  A  A  P  E  E  H  L  F  L

22621  CGTCGGCATCCCGCACATCACCGCGGACCTGTGGTCCGCGACCCTGCTCAACGACGAGCT  22680
        V  G  I  P  H  I  T  A  D  L  W  S  A  T  L  L  N  D  E  L

22681  CATGGCGCACTACAGGGCGGGGGCCGAGGGGACTCCCTCCCGGGCCCCCACCCCCGTCGC  22740
        M  A  H  Y  R  A  G  A  E  G  T  P  S  R  A  P  T  P  V  A

22741  GCAGTACGCCGACTTCGCGCAGTGGCAGCGCGCGTGGTGGAACCGGGACCGCACCGAGCG  22800
        Q  Y  A  D  F  A  Q  W  Q  R  A  W  W  N  R  D  R  T  E  R

22801  GGAGGCCGGACGGTGGCGGGCGCGGCTGGACGGGCTGTCCGCCGTGGAACTGCCCCTGGA  22860
        E  A  G  R  W  R  A  R  L  D  G  L  S  A  V  E  L  P  L  D

22861  CCGGCCCCGCCCCGCGGGCCGCCGGCGGGACTGCTTCCTGATCGGGGACACCTTCGACGC  22920
        R  P  R  P  A  G  R  R  R  D  C  F  L  I  G  D  T  F  D  A

22921  CGAACTGAGCGACCGGCTGCGCGCCTTGGCACGCACCGCCGACGTCACGCTGTACGTGGT  22980
        E  L  S  D  R  L  R  A  L  A  R  T  A  D  V  T  L  Y  V  V

22981  GCTGCTGGCGGCGTTCCACTGGCTGGTGGGGCGGATGTCGGGCGCCGGCCGGCTGGTGAC  23040
        L  L  A  A  F  H  W  L  V  G  R  M  S  G  A  G  R  L  V  T

23041  CACCTCGCTCGTGGCCGCCCGGCACGGCAGCGCGGTACAGGGGATGACCGGCCCGTTCTC  23100
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          T  S  L  V  A  A  R  H  G  S  A  V  Q  G  M  T  G  P  F  S
                .     .     .     .     .     .     .     .     .
23101  GGACTACCTGGCCCTGGTCGGGGACCTGTCGGGCGATCCGGACTTCCTGGAGTCCCTGCG  23160
          D  Y  L  A  L  V  G  D  L  S  G  D  P  D  F  L  E  S  L  R
                .     .     .     .     .     .     .     .     .
23161  CCGCGTACGCGACGAGTGCCTGACCGCCCACGACCACCAGCGGCTTCCGTTCTCACAGGT  23220
          R  V  R  D  E  C  L  T  A  H  D  H  Q  R  L  P  F  S  Q  V
                .     .     .     .     .     .     .     .     .
23221  CCTCGAAGTCATGGACCCCGGACGCGAGTTGCACCCCCATCCGCTGGAGCAGCTCGGGTT  23280
          L  E  V  M  D  P  G  R  E  L  H  P  H  P  L  E  Q  L  G  F
                .     .     .     .     .     .     .     .     .
23281  CAACCTCCACAACATCCCTCCCGCGGTCATGGACTTCTCCGGCGACGTCGTCGTCTCGGC  23340
          N  L  H  N  I  P  P  A  V  M  D  F  S  G  D  V  V  V  S  A
                .     .     .     .     .     .     .     .     .
23341  GGTGAACCCGGAGGGGGACGACGGGGAGAGCGGCGACGGGGAGTACGTGCCCTGGACCGC  23400
          V  N  P  E  G  D  D  G  E  S  G  D  G  E  Y  V  P  W  T  A
                .     .     .     .     .     .     .     .     .
23401  CGACCTGACCTTCGACGTCTACGACTACGGCACCGGCCATATGCCGTTCGACGTGATACT  23460
          D  L  T  F  D  V  Y  D  Y  G  T  G  H  M  P  F  D  V  I  L
                .     .     .     .     .     .     .     .     .
23461  CGACCGGCGGCTGGCCGATCCGGCGACGGCCCGGGAGTGGGCCGGGCACTACCGGTCGGT  23520
          D  R  R  L  A  D  P  A  T  A  R  E  W  A  G  H  Y  R  S  V
                .     .     .     .     .     .     .     .     .
23521  GCTCCGTGCGGTCGTCGCCGACCCCGGCGTGCGCCTGTCCGCCCTCGGCACCCTGCTGTC  23580
          L  R  A  V  V  A  D  P  G  V  R  L  S  A  L  G  T  L  L  S
                .     .     .     .     .     .     .     .     .
23581  CCTGCCGCGACCGCCGTCCGCCACGTCCTTCGGCGGCCGGGAGATCGACGTCCGGCGCGT  23640
          L  P  R  P  P  S  A  T  S  F  G  G  R  E  I  D  V  R  R  V
                .     .     .     .     .     .     .     .     .
23641  CGAACGCGAGTTGGCGGGGCGCGACGGGATCACCGCCGCCCTGGTCGCGGTGGCGCCCCG  23700
          E  R  E  L  A  G  R  D  G  I  T  A  A  L  V  A  V  A  P  R
                .     .     .     .     .     .     .     .     .
23701  GCGCCTGGCCACCGGGCTGCGCGTACGGGAACTGGTCGCCTACTGCGCCGTCGAGGGCAC  23760
          R  L  A  T  G  L  R  V  R  E  L  V  A  Y  C  A  V  E  G  T
                .     .     .     .     .     .     .     .     .
23761  GCCGCGTCCGAACGCGGCCCACGACATCCGCGGCCGCCTGCGGGAGCGCCTGCCCGACGG  23820
          P  R  P  N  A  A  H  D  I  R  G  R  L  R  E  R  L  P  D  G
                .     .     .     .     .     .     .     .     .
23821  CTGGGTGCCGACCGTGTTCGTCGAGCGCCCGCCGGAGGAGATCCGGAAGGCCCTGGCCGC  23880
          W  V  P  T  V  F  V  E  R  P  P  E  E  I  R  K  A  L  A  A
                .     .     .     .     .     .     .     .     .
23881  CCGGGCGGCGGGCGGCGAACGGGCGGAGCCGCTGCCGCCGCCCGAGGACTGCGTCCCGCT  23940
          R  A  A  G  G  E  R  A  E  P  L  P  P  P  E  D  C  V  P  L
                .     .     .     .     .     .     .     .     .
23941  TCCCGAGGAGGGCCGGCCCCCCTCGGACCCGTCCGAGCGGCGGCTGGCCGCGCTCTGGGC  24000
          P  E  E  G  R  P  P  S  D  P  S  E  R  R  L  A  A  L  W  A
                .     .     .     .     .     .     .     .     .
24001  CGAGATCCTGGGCGCCCCGCCGAAGAGCGTGACCGAGCCCTTCTTCCGCGTCGGCGTCAC  24060
          E  I  L  G  A  P  P  K  S  V  T  E  P  F  F  R  V  G  V  T
                .     .     .     .     .     .     .     .     .
24061  CGATAAGGACGCCCTCCGCTTCCTGGCCCGCGTGGCGGAGGACTTCGGCGTCACCGTGCC  24120
          D  K  D  A  L  R  F  L  A  R  V  A  E  D  F  G  V  T  V  P
                .     .     .     .     .     .     .     .     .
24121  CTTCGCCGACTTCCTCAGCGCTCCCAACCTGCGTATGGTGAAGGACAATTTGGCTGAGAA  24180
          F  A  D  F  L  S  A  P  N  L  R  M  V  K  D  N  L  A  E  K
                .     .     .     .     .     .     .     .     .
24181  ACGGAGGGTGTAACGCGCAATGAGTGAGTGGTAGGGTCGGAATCGAACCGCACTGATCGG  24240
          R  R  V  *
                .     .     .     .     .     .     .     .     .
24241  CAATCTTTTCGGTCAGCTGTTCCGGATATTCCGGGGCGCGTCGGCGCTCCCTCGACCAAG  24300
                .     .     .     .     .     .     .     .     .
24301  GGCGTACGCGGATAAGCGTGCGCCGCCCCACGGCTGCGTCTCGACGCCTTCATCGGCGCG  24360
                .     .     .     .     .     .     .     .     .
24361  TCGGACACTTCGCGGTGCCAGTCGGCACGCTCAGAGATCAGTGGAATGCCTCGGTGTGCC  24420
                                                   M  P  R  C  A    (orf26)
                .     .     .     .     .     .     .     .     .
24421  CGAGGTGCGCTCAGTACTGCTGTCCACACAACGCGCCAAGGGAGTTGGAACGTGATGGAG  24480
          R  G  A  L  S  T  A  V  H  T  T  R  Q  G  S  W  N  V  M  E
                .     .     .     .     .     .     .     .     .
24481  ACGGCGAATTCCGGCTATCGGGTCTCACCTCAGCAGCGGCATTTATGGGCCATGCTGACC  24540
          T  A  N  S  G  Y  R  V  S  P  Q  Q  R  H  L  W  A  M  L  T
                .     .     .     .     .     .     .     .     .
24541  CGCGGGCGGGACGGCGGGCGACGTGCGTTCACCCAGTCCGCCGTGGTGGTCGACCGTTCC  24600
          R  G  R  D  G  G  R  R  A  F  T  Q  S  A  V  V  V  D  R  S
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24601 CTGGACGCCGCACGTCTGCGCGCCGCGCTGGCCTCCGTGGTGGCCGCCCACGAGCCGCTG 24660
      L  D  A  A  R  L  R  A  A  L  A  S  V  V  A  A  H  E  P  L

24661 CGGACGACCTTCACCGGTCTCGCGGGACGGACCGCGCCGGTCCAGGTCGTCCATGACCCG 24720
      R  T  T  F  T  G  L  A  G  R  T  A  P  V  Q  V  V  H  D  P

24721 GACGAGCAGCCGCTGTCCGTCGTCGACCTGCCGCCCTCGTGCGCCGACGGCTCGGGCCCG 24780
      D  E  Q  P  L  S  V  V  D  L  P  P  S  C  A  D  G  S  G  P

24781 GAACTGGACGAGCTCCGGCTCCGCGAACGCGCCGCCCTCGACCCGCGCGGCGGGCCCGTC 24840
      E  L  D  E  L  R  L  R  E  R  A  A  L  D  P  R  G  G  P  V

24841 TTCCGGGCCGCCCTGGCGCGGGCCGGCGAGGACCGGGCGGTGCTGGTGCTCACCGCGCAC 24900
      F  R  A  A  L  A  R  A  G  E  D  R  A  V  L  V  L  T  A  H

24901 GCCCTGGTCGCGGACCGGCTCTCCCTCCGGCTGCTGGCCGGGCAGATCCTCGCGGCGTAC 24960
      A  L  V  A  D  R  L  S  L  R  L  L  A  G  Q  I  L  A  A  Y

24961 AGCGGGGAGACCGTGTCCCCCGATGGCCCGCCGCCCTTGCAGTACGCCGACTTCGCCGCC 25020
      S  G  E  T  V  S  P  D  G  P  P  P  L  Q  Y  A  D  F  A  A

25021 TGGCACCACGACCTGCTCACCGCCGAGGACGCCGCCCCCGACCGCGCGCACTGGGCCGCC 25080
      W  H  H  D  L  L  T  A  E  D  A  A  P  D  R  A  H  W  A  A

25081 CACACCGCCACCGCCGGCACCGGGCCGCTCCCCGGCGTCGTACGGCCCGGCGCCGCCCCG 25140
      H  T  A  T  A  G  T  G  P  L  P  G  V  V  R  P  G  A  A  P

25141 GGTCCGTGGCGGGCGCGGGAGTGGGAACTGCCCGCCGAACTGGTGGCGGGGATCGACGGC 25200
      G  P  W  R  A  R  E  W  E  L  P  A  E  L  V  A  G  I  D  G

25201 GTCGCCGGGAAGCTGTCCACCGATCCCGCCACCGTGCTGCACGCCGCCTTCCGTATCGCG 25260
      V  A  G  K  L  S  T  D  P  A  T  V  L  H  A  A  F  R  I  A

25261 GTCTGGCGGCTCGCCGGCGAGCGGAACCTGCCCGTCGCCCTCACTCGTGACGGCCGTTCC 25320
      V  W  R  L  A  G  E  R  N  L  P  V  A  L  T  R  D  G  R  S

25321 CACCCCGAACTCCGCACCGCGATCGGCGCCTTCGAGCGTGAGCTCCCGCTCGTCCACGAG 25380
      H  P  E  L  R  T  A  I  G  A  F  E  R  E  L  P  L  V  H  E

25381 ATCCGTCACGAGACGGCGTTCGCGGAATACGCGCGCGCTCTGGACGCGCTCGTCGCCGAG 25440
      I  R  H  E  T  A  F  A  E  Y  A  R  A  L  D  A  L  V  A  E

25441 GGCGAGGAACTCCTCGACCATTGCGACCCGGAACTGCTCGGCAGCCTCGACGGCACCGCG 25500
      G  E  E  L  L  D  H  C  D  P  E  L  L  G  S  L  D  G  T  A

25501 GAAGGGCCCTGCTTCACCTTCACCCACCACCAGGCCGAAACACCGGTCCGGCGGGCCGGC 25560
      E  G  P  C  F  T  F  T  H  H  Q  A  E  T  P  V  R  R  A  G

25561 ATCACCTTTACCACCGTCCATCAGGATTCGGGTACGCCGATTCCCGTCCGCCTGACCGCC 25620
      I  T  F  T  T  V  H  Q  D  S  G  T  P  I  P  V  R  L  T  A

25621 CGACGCGACGGCGCCCGGCTGCGCATGGAACTGGGATACGACGAGGGCCGTATCGACGAG 25680
      R  R  D  G  A  R  L  R  M  E  L  G  Y  D  E  G  R  I  D  E

25681 ACGTTTCCCGAGAACGCCGCCGCCTGCCTCACCCGCATTCTCGAAGGCGTCGTCTCCGCC 25740
      T  F  P  E  N  A  A  A  C  L  T  R  I  L  E  G  V  V  S  A

25741 CCCGAGGGCCCGGTCGGCGACATCCGCATGCTGTCGGACGAGACCGCACGGCTGCTCCGG 25800
      P  E  G  P  V  G  D  I  R  M  L  S  D  E  T  A  R  L  L  R

25801 GAAGCGGGGCTGGGCCCCCGCGTGGAACTTCCCGGCAAGGCGGTCCACGAACTCTTCGCC 25860
      E  A  G  L  G  P  R  V  E  L  P  G  K  A  V  H  E  L  F  A

25861 GAGCAGGCCGCGCGCACCCCCGGGGCGGTCGCGGTCAGCGCGGGCGAGGACGCCCTCACG 25920
      E  Q  A  A  R  T  P  G  A  V  A  V  S  A  G  E  D  A  L  T

25921 TACGCCGAACTCGACGAGCGGTCCAACCGCCTGGCACACCACCTGACCGGGCTCGGGGTG 25980
      Y  A  E  L  D  E  R  S  N  R  L  A  H  H  L  T  G  L  G  V

25981 ACACCCGGCCGGCACGTCGTGGTCTCGGTCGGCCGCTCCGCCGAGCTGCTCGTCGGGCTG 26040
      T  P  G  R  H  V  V  V  S  V  G  R  S  A  E  L  L  V  G  L

26041 CTCGGCGTGCTCAAGGCGGGTGGCGCCTTCGTCCCCGTCGACGTGGGCTTCCCCCGCAAA 26100
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        L  G  V  L  K  A  G  G  A  F  V  P  V  D  V  G  F  P  R  K
                .     .     .     .     .     .     .     .     .
26101   CGGCTGGAGTTCGTGCTCCGGGAGACCGCCGCGCCGGTCCTGCTCTGCACCGCCGACGTA   26160
        R  L  E  F  V  L  R  E  T  A  A  P  V  L  L  C  T  A  D  V
                .     .     .     .     .     .     .     .     .
26161   CGGGACCGCATCGGCACTCGGACCCTCGACGACGCCGGGGGTGACACCCGTCGCGCTGGAC   26220
        R  D  R  I  G  T  R  T  L  D  D  A  G  V  T  P  V  A  L  D
                .     .     .     .     .     .     .     .     .
26221   GCCGACCGGCGGCGCATCGCCGCACACCCCGCCGGCCCCACCGGCATCGCCACCACCCCC   26280
        A  D  R  R  R  I  A  A  H  P  A  G  P  T  G  I  A  T  T  P
                .     .     .     .     .     .     .     .     .
26281   GACGCCCCCGCGTACGTCGTCTACACCTCCGGCACCACCGGGAAGCCCAACGGCGTACGC   26340
        D  A  P  A  Y  Y  V  V  Y  T  S  G  T  T  G  K  P  N  G  V  R
                .     .     .     .     .     .     .     .     .
26341   GTCCCGCACCGGGGCCTCACCAACTACCTCACCTGGTGCACCGGCGCCTACGGACTCGAC   26400
        V  P  H  R  G  L  T  N  Y  L  T  W  C  T  G  A  Y  G  L  D
                .     .     .     .     .     .     .     .     .
26401   GGGGGCACCGGCACCCTCGTGCACACCTCCATCAGCTTCGACCTCACCCTCACCACCCTG   26460
        G  G  T  G  T  L  V  H  T  S  I  S  F  D  L  T  L  T  T  L
                .     .     .     .     .     .     .     .     .
26461   TTCGGCCCCCTGCTCGCCGGCGGGCAGGTGGTCATGCTCTCCGAGACCGCCGGCGTGACC   26520
        F  G  P  L  L  A  G  G  Q  V  V  M  L  S  E  T  A  G  V  T
                .     .     .     .     .     .     .     .     .
26521   GGCCTGATCGCCGCGCTGCGCTCCCGGCGCGACCTCACCCTGGTCAAGCTGACCCCGACC   26580
        G  L  I  A  A  L  R  S  R  R  D  L  T  L  V  K  L  T  P  T
                .     .     .     .     .     .     .     .     .
26581   CACCTCGACGTCGTCAACCAGCTGCTCACCCCCGACGAGCTGCGCGGCGCGGTCCGCACC   26640
        H  L  D  V  V  N  Q  L  L  T  P  D  E  L  R  G  A  V  R  T
                .     .     .     .     .     .     .     .     .
26641   CTCGTCGTCGGCGGGGAGGCGGTGCGGGCGGAGAGCCTGGAGCCGTTCCGGGCCTCCGGG   26700
        L  V  V  G  G  E  A  V  R  A  E  S  L  E  P  F  R  A  S  G
                .     .     .     .     .     .     .     .     .
26701   ACGCGGGTCGTCAACGAGTACGGGCCCAGCGAGACGGTCGTCGGCAGCGTCGCGCACGTC   26760
        T  R  V  V  N  E  Y  G  P  S  E  T  V  V  G  S  V  A  H  V
                .     .     .     .     .     .     .     .     .
26761   GTCGACGCCGCCACGCCCCGTACCGGCCCGGTGCCCATCGGCCGGCCGATCGCCAACACC   26820
        V  D  A  A  T  P  R  T  G  P  V  P  I  G  R  P  I  A  N  T
                .     .     .     .     .     .     .     .     .
26821   ACCGTCCACCTGCTCGACCAGCGGCGGCGGCCCGTCCCCGACGGCGTCGTCGGCGAGCTG   26880
        T  V  H  L  L  D  Q  R  R  R  P  V  P  D  G  V  V  G  E  L
                .     .     .     .     .     .     .     .     .
26881   TGGATCGGCGGCGCCGGTGTCGCCGACGGCTACCTGGGGCGGCCGGAACTCACCGGCGAG   26940
        W  I  G  G  A  G  V  A  D  G  Y  L  G  R  P  E  L  T  G  E
                .     .     .     .     .     .     .     .     .
26941   CGCTTCCTCCCCAGCGACTACCCGCCGGACGGCGGCCGGGTCTACCGCACCGGCGACCTG   27000
        R  F  L  P  S  D  Y  P  P  D  G  G  R  V  Y  R  T  G  D  L
                .     .     .     .     .     .     .     .     .
27001   GCCCGCCGGCGCGCCGACGGCACCCTGGAGTACCTCGGGCGCACCGACGCGCAGGTGAAG   27060
        A  R  R  R  A  D  G  T  L  E  Y  L  G  R  T  D  A  Q  V  K
                .     .     .     .     .     .     .     .     .
27061   ATCCGCGGCGTCCGGGTGGAGCCCGCCGAGACCGAGGCCGTCCTCGCCTCCCACCCCGGC   27120
        I  R  G  V  R  V  E  P  A  E  T  E  A  V  L  A  S  H  P  G
                .     .     .     .     .     .     .     .     .
27121   GTCGGCCAGGCCGTCGTGGTCGCCCGGCTGGACGAGGACCCCGGCCGTTCGTCGCCGCTC   27180
        V  G  Q  A  V  V  V  A  R  L  D  E  D  P  G  R  S  S  P  L
                .     .     .     .     .     .     .     .     .
27181   GCCGGCGAGCTGACGCTGACCGGCTACGTGGTCCCGGCCCGCGGTGCCCAGGCGCCCCCG   27240
        A  G  E  L  T  L  T  G  Y  V  V  P  A  R  G  A  Q  A  P  P
                .     .     .     .     .     .     .     .     .
27241   CACGAGGAGCTCATCGCGTACTGCCGGGAGCGGCTGCCCGAGCACTTCGTCCCGGCCGTC   27300
        H  E  E  L  I  A  Y  C  R  E  R  L  P  E  H  F  V  P  A  V
                .     .     .     .     .     .     .     .     .
27301   CTCGTCACCCTCGACGCCCTGCCCGTCACCGGCCACGGCAAGATCGACCGCGGTGCGCTG   27360
        L  V  T  L  D  A  L  P  V  T  G  H  G  K  I  D  R  G  A  L
                .     .     .     .     .     .     .     .     .
27361   CCCAAGCCGCACGCCCGGGCCCGGGACGGCGCGGCGTACGTCGCGCCGCGCACCGCCACC   27420
        P  K  P  H  A  R  A  R  D  G  A  A  Y  V  A  P  R  T  A  T
                .     .     .     .     .     .     .     .     .
27421   GAGGAGATCCTCGCGGCCACCGTCGCGAAGGTGCTGGGCGTCGAGCGCGTCGGCATCGAC   27480
        E  E  I  L  A  A  T  V  A  K  V  L  G  V  E  R  V  G  I  D
                .     .     .     .     .     .     .     .     .
27481   GACAACTACTTCGTCCTGGGCGGCGACTCCATCCGCAGCGTCATGGTCGCCAGCCGGGCC   27540
        D  N  Y  F  V  L  G  G  D  S  I  R  S  V  M  V  A  S  R  A
                .     .     .     .     .     .
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27541  CAGGCCCGCGGGGTCGAGGTCACCGTGGCCGACCTGCACCGGCACCCCACCGTCCGGGCC  27600
       Q  A  R  G  V  E  V  T  V  A  D  L  H  R  H  P  T  V  R  A

27601  TGCGCCGCGCACCTGGACGCCCGCGAGGACCTGCCGCGGACGCCCGTCACCGAACCCTTC  27660
       C  A  A  H  L  D  A  R  E  D  L  P  R  T  P  V  T  E  P  F

27661  GCGCTGATCTCCGCCGAGGACCGGGCGCTGGTGCCGGACGACGTCGAGGACGCCTTCCCG  27720
       A  L  I  S  A  E  D  R  A  L  V  P  D  D  V  E  D  A  F  P

27721  CTGAACCTGCTCCAGGAAGGCATGATCTTCCACCGCGACTTCGCGGCGAAGTCGGCCGTC  27780
       L  N  L  L  Q  E  G  M  I  F  H  R  D  F  A  A  K  S  A  V

27781  TACCACGCCATCGCGTCCGTGCGGCTGCGCGCCCCGTTCGACCTCGCCGTGCTGCGGATG  27840
       Y  H  A  I  A  S  V  R  L  R  A  P  F  D  L  A  V  L  R  M

27841  GTCGTGCGCCAGCTCGTCGAGCGGCACCCGATGCTGCGCACCTCCTTCGACATGAGCCGC  27900
       V  V  R  Q  L  V  E  R  H  P  M  L  R  T  S  F  D  M  S  R

27901  TTCAGCCGCCCGCTGCAACTGGTGCACCGCGAGTTCGCCGATCCGCTGCACTACGAGGAC  27960
       F  S  R  P  L  Q  L  V  H  R  E  F  A  D  P  L  H  Y  E  D

27961  CTGCGCGGCAGGAGCGCCGAGGAGCAGGACGCCCGCGTCGAGGAGTGGATCGAGCGGGAG  28020
       L  R  G  R  S  A  E  E  Q  D  A  R  V  E  E  W  I  E  R  E

28021  AAGGAACGCGGCTTCGAGCTGCACGAGTTCCCGCTGATCCGCTTCATGGCGCAGCGCCTG  28080
       K  E  R  G  F  E  L  H  E  F  P  L  I  R  F  M  A  Q  R  L

28081  GAGGACGACGTCTTCCAGTTCACCTACGGCTTCCACCACGAGATCGTGGACGGCTGGAGC  28140
       E  D  D  V  F  Q  F  T  Y  G  F  H  H  E  I  V  D  G  W  S

28141  GAAGCCCTGATGATCACCGAGCTGTTCAGCCACTACTTCTCGGTGATCTACGACGAGCCG  28200
       E  A  L  M  I  T  E  L  F  S  H  Y  F  S  V  I  Y  D  E  P

28201  ATCGCGATCAAGCCACCCACCGCCGGCATGCGCGACGCCGTCGCCCTGGAGCTGGAGGCC  28260
       I  A  I  K  P  P  T  A  G  M  R  D  A  V  A  L  E  L  E  A

28261  CTCGCGGACCGCCGCAACTACGAGTTCTGGGACTCCTACCTCGCCGACGCCACCCTGATG  28320
       L  A  D  R  R  N  Y  E  F  W  D  S  Y  L  A  D  A  T  L  M

28321  CGGCTGCCCAGGCCCGGCACCGGACCCCGGGCCGACAAGGGCGACCGGGACATCACCCGC  28380
       R  L  P  R  P  G  T  G  P  R  A  D  K  G  D  R  D  I  T  R

28381  ATCGCCGTCCCCGTCCCCACCGAACTCTCCGACGGCCTCAAGCGGGTCGCCGCCACCCAC  28440
       I  A  V  P  V  P  T  E  L  S  D  G  L  K  R  V  A  A  T  H

28441  GCCGTCCCGCTGAAGACCGTGCTCCTGGCCGCGCACATGGTGGTGATGTCCCTCTACGGC  28500
       A  V  P  L  K  T  V  L  L  A  A  H  M  V  V  M  S  L  Y  G

28501  GGCCACGAGGACACCCTCACCTACACCGTCACCAACGGCCGCCCCGAGACCGCCGACGGC  28560
       G  H  E  D  T  L  T  Y  T  V  T  N  G  R  P  E  T  A  D  G

28561  AGCACCGCGATCGGGCTGTTCGTCAACAGCCTCGCGCTCCGCGTCCGGATGACCGGCGGC  28620
       S  T  A  I  G  L  F  V  N  S  L  A  L  R  V  R  M  T  G  G

28621  ACCTGGGCCGACCTGATCACCGCCACGCTGGAGTCCGAGCGCGCCTCGATGCCGTACCGG  28680
       T  W  A  D  L  I  T  A  T  L  E  S  E  R  A  S  M  P  Y  R

28681  CGGCTGCCGATGGCCGAACTCAAGCGCCACCAGGGCAACGAACCCCTGGCCGAGACGCTG  28740
       R  L  P  M  A  E  L  K  R  H  Q  G  N  E  P  L  A  E  T  L

28741  TTCTTCTTCACCAACTACCACGTCTTCCACGTGCTCGACCGCTGGATCGACCGCGGCGTC  28800
       F  F  F  T  N  Y  H  V  F  H  V  L  D  R  W  I  D  R  G  V

28801  GGCCACGTCGCCAACGAGCTCTACGGCGAGTCCACCTTCCCCTTCTGCGGCATCTTCCGC  28860
       G  H  V  A  N  E  L  Y  G  E  S  T  F  P  F  C  G  I  F  R

28861  CTGAACCGGGAGACCGGCGAGCTGGAGGTCCGCATCGAGTACGACAGCCTGCAGTTCTCC  28920
       L  N  R  E  T  G  E  L  E  V  R  I  E  Y  D  S  L  Q  F  S

28921  GACGCCCTCATGGAGAGCGTCCGCGACAGCTACGCCCGCGTCCTCGCGGCCCTGGTCGCC  28980
       D  A  L  M  E  S  V  R  D  S  Y  A  R  V  L  A  A  L  V  A

28981  GACCCCGACGGGCGCTACGACCGGCACGAGTTCCGCTCCGACCGCGACCGGGCCGCACTG  29040
       D  P  D  G  R  Y  D  R  H  E  F  R  S  D  R  D  R  A  A  L
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29041 GCCGTCCTCACCCGCGGGCCCGAGGCGCCGGCGGCCGACCGGTGCCTGCACGACCTGGTG 29100
      A  V  L  T  R  G  P  E  A  P  A  A  D  R  C  L  H  D  L  V

29101 GCGGACCGGGCGGCGGACCGCCCCGACGCCCCGGCCGTCCAGCTGGACACCGACGTGCTC 29160
      A  D  R  A  A  D  R  P  D  A  P  A  V  Q  L  D  T  D  V  L

29161 AGCTACGGCGAGCTCGACCGCCGCGCCAACCGGCTGGCCCACCACCTGCGTTCGCTCGGC 29220
      S  Y  G  E  L  D  R  R  A  N  R  L  A  H  H  L  R  S  L  G

29221 ATCGGCCCGGAGAGCGTCGTCGGCGTCCTGGCCGAACGCTCCCTCGCCCAGATCATCGGC 29280
      I  G  P  E  S  V  V  G  V  L  A  E  R  S  L  A  Q  I  I  G

29281 CTCCTCGCGGTCCTCAAGGCGGGCGCCGCCTACGTCCCGCTCGACCCGGCCCAGCCCGAC 29340
      L  L  A  V  L  K  A  G  A  A  Y  V  P  L  D  P  A  Q  P  D

29341 GAGCGCCTCGCCGCCGTCATCGCCGGGAGCGGGGCCGCCGCCGTCCTCCACCGGCCCGGC 29400
      E  R  L  A  A  V  I  A  G  S  G  A  A  A  V  L  H  R  P  G

29401 CTCGAAGGGCGGCTGCCCGCGGGCGTCCGCGCGCTCCCCACCGACGCCGCCGACGGCAGC 29460
      L  E  G  R  L  P  A  G  V  R  A  L  P  T  D  A  A  D  G  S

29461 ACCGCCACGCACGACCCCGGGCCCACCGCCACGCCCCGCAACGCCGCGTACGTGATGTAC 29520
      T  A  T  H  D  P  G  P  T  A  T  P  R  N  A  A  Y  V  M  Y

29521 ACCTCCGGATCCACCGGAGAGCCCAAGGGCATCGTCGTCGAACACCGCAACGTCGTGGCC 29580
      T  S  G  S  T  G  E  P  K  G  I  V  V  E  H  R  N  V  V  A

29581 TCCCTCGCCGCCCGCGGCGCCCACTACGCGGCCGGACCCGGCCGGTTCCTGCTGCTGTCC 29640
      S  L  A  A  R  G  A  H  Y  A  A  G  P  G  R  F  L  L  L  S

29641 TCCTTCGCCTTCGACAGCTCGGTCGCCGGCATCTTCTGGACGCTGACCCAGGGCGGCACC 29700
      S  F  A  F  D  S  S  V  A  G  I  F  W  T  L  T  Q  G  G  T

29701 CTCGTCCTGCCCGGCGAGGGACAGCAACTCGACCCCGCCGCGCTGGTGGAGACCATCGCC 29760
      L  V  L  P  G  E  G  Q  Q  L  D  P  A  A  L  V  E  T  I  A

29761 CGGCAACGGCCCACCCACACCCTCGCCATCCCCTCCCTGCTGGCGCCCGTCCTGGACCAG 29820
      R  Q  R  P  T  H  T  L  A  I  P  S  L  L  A  P  V  L  D  Q

29821 GCCGCCCCCGGCGACCTCGCCTCCCTGCGCACGGTGATCGCCGCGGGCGAGTCCTGTCCG 29880
      A  A  P  G  D  L  A  S  L  R  T  V  I  A  A  G  E  S  C  P

29881 GCCGAACTGGCCGCCGCCTGCCGGGACCTGCTGCCCGGGAGCACCTTCCACAACGAGTAC 29940
      A  E  L  A  A  A  C  R  D  L  L  P  G  S  T  F  H  N  E  Y

29941 GGCCCCACCGAGACCACCGTGTGGAGCACCGTCTGGTCCCAGGAGAACGAGCACGACGGA 30000
      G  P  T  E  T  T  V  W  S  T  V  W  S  Q  E  N  E  H  D  G

30001 CCCCACCTCCCCATCGGCCGGCCGGTCGCGGGCACCTGGGTGCACCCCCGCGACCACCGC 30060
      P  H  L  P  I  G  R  P  V  A  G  T  W  V  H  P  R  D  H  R

30061 GGACGCACCGTCCCCCTCGGCGTCGCCGGCGAACTCTCCATCGGCGGCGCCGGCGTGGCC 30120
      G  R  T  V  P  L  G  V  A  G  E  L  S  I  G  G  A  G  V  A

30121 CGCGGCTACCTCGGGCGCCCCCGGGACACCGCGGCCGCCTTCCGCCCCGACCCCGAGGCC 30180
      R  G  Y  L  G  R  P  R  D  T  A  A  A  F  R  P  D  P  E  A

30181 ACGGCTCCCGGCGGCCGCGCCTACGCCACCGGCGACCTCGGCCGCTACCTCCCCGACGGC 30240
      T  A  P  G  G  R  A  Y  A  T  G  D  L  G  R  Y  L  P  D  G

30241 AACCTGGAGTTCCTCGGCCGCGCCGACCACCAGGTCAAGATCCGCGGCTTCCGGGTCGAG 30300
      N  L  E  F  L  G  R  A  D  H  Q  V  K  I  R  G  F  R  V  E

30301 CTCGGCGAGATCGAGGCCGTCCTCGACACCCACCCGGAGCTCCAGCGGACCATCGTCATG 30360
      L  G  E  I  E  A  V  L  D  T  H  P  E  L  Q  R  T  I  V  M

30361 GCACGCGGCGACCACCCCGGCGACCAGGTGCTCGTCGCCTACGTCCTCCCCGCCCCCGGC 30420
      A  R  G  D  H  P  G  D  Q  V  L  V  A  Y  V  L  P  A  P  G

30421 CGGCGGCCCGAACCCGCCGACATCCAGGGGTACGTCCGCGACCGGCTGCCCCGCTACATG 30480
      R  R  P  E  P  A  D  I  Q  G  Y  V  R  D  R  L  P  R  Y  M

30481 GTGCCCACCGCGGTGATCGTCCTCGACGCGGTACCGCTGACCGCCGCCGGCAAGGTCGAC 30540
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        V  P  T  A  V  I  V  L  D  A  V  P  L  T  A  A  G  K  V  D
      .     .     .     .     .     .     .     .     .     .     .
30541 CGGGCCTCGCTCCCCGCCCCCAGCCACGCCCAGCTCACCCGGGACCAGGAGTACGTCGAG 30600
        R  A  S  L  P  A  P  S  H  A  Q  L  T  R  D  Q  E  Y  V  E
      .     .     .     .     .     .     .     .     .     .     .
30601 CCCGGCACCGACACCGAGCGGGCGCTCGCCGCCATCTGGGCCGACGTCCTCAAACTGGAC 30660
        P  G  T  D  T  E  R  A  L  A  A  I  W  A  D  V  L  K  L  D
      .     .     .     .     .     .     .     .     .     .     .
30661 CGGATCGGGGCCGGTGACCGCTTCTTCGACGTCGGCGGCGAATCCCTGCGCGCGATGCAG 30720
        R  I  G  A  G  D  R  F  F  D  V  G  G  E  S  L  R  A  M  Q
      .     .     .     .     .     .     .     .     .     .     .
30721 GCCACCGCCGCGGCCAACAAGATGTTCCGCACCCGCGTCTCCGTCCGCCGCCTCTTCGAG 30780
        A  T  A  A  A  N  K  M  F  R  T  R  V  S  V  R  R  L  F  E
      .     .     .     .     .     .     .     .     .     .     .
30781 GCGCCCTCCCTGCGGGAGTTCGCCCACGAGATCGACAAGGCCCGCCTCGCGGGCGGCGGG 30840
        A  P  S  L  R  E  F  A  H  E  I  D  K  A  R  L  A  G  G  G
      .     .     .     .     .     .     .     .     .     .     .
30841 ACCGGCCTCACCGGCCCCGCGGCCGCCCCGGCCACCGGAGGTGCCGCCGAATGACCCCGG 30900
        T  G  L  T  G  P  A  A  A  P  A  T  G  G  A  A  E  *
                                                   M  T  P  A  (orf25)
      .     .     .     .     .     .     .     .     .     .     .
30901 CCGCCGACACCACCCACCCGCTCTCGCCGGCCCAGCGCAGCATGTGGTTCCTGCACCGGC 30960
          A  D  T  T  H  P  L  S  P  A  Q  R  S  M  W  F  L  H  R  L
      .     .     .     .     .     .     .     .     .     .     .
30961 TCGCGCCCGAGGTGCCCGCCTACAACATCTGCACCGCCATCGAGCTCACCGGCACACCGC 31020
          A  P  E  V  P  A  Y  N  I  C  T  A  I  E  L  T  G  T  P  R
      .     .     .     .     .     .     .     .     .     .     .
31021 GCCCGGCGGCGCTGCGGGACGTGGTACGGCGGCTCGGCCGCAGGCACGAGGCGCTGCGCA 31080
          P  A  A  L  R  D  V  V  R  R  L  G  R  R  H  E  A  L  R  T
      .     .     .     .     .     .     .     .     .     .     .
31081 CGGTGTTCCCGTCGGTGGGGGAGACCCCCCGCCAACGGGTCACCGACCGGGCGGCGCCCC 31140
          V  F  P  S  V  G  E  T  P  R  Q  R  V  T  D  R  A  A  P  L
      .     .     .     .     .     .     .     .     .     .     .
31141 TGCGGACCGTGGACCTCACCCACCTGACCCCCGCCGCCGCCGAGGCCGAGACCGCACGGA 31200
          R  T  V  D  L  T  H  L  T  P  A  A  A  E  A  E  T  A  R  T
      .     .     .     .     .     .     .     .     .     .     .
31201 CGCTACGGTGCGCCGCCGCCCGGCCGTTCCGGCTCGACACCGGCCCCCTGGCGGAATGGA 31260
          L  R  C  A  A  A  R  P  F  R  L  D  T  G  P  L  A  E  W  T
      .     .     .     .     .     .     .     .     .     .     .
31261 CCCTGCTGCGCCGCGCCCCCGGCCACGCGCTGCTCGTCCTCTCCGTCCACCACATCGTCT 31320
          L  L  R  R  A  P  G  H  A  L  L  V  L  S  V  H  H  I  V  F
      .     .     .     .     .     .     .     .     .     .     .
31321 TCGACGGCGGCTCGCTCCACGTGGTCTGCCGCGAACTGGAGGAGGCGTACGGAGCGGCCC 31380
          D  G  G  S  L  H  V  V  C  R  E  L  E  E  A  Y  G  A  A  L
      .     .     .     .     .     .     .     .     .     .     .
31381 TCGCCGGGCGCCCGGACCCCCTCGGCACACCCGCGCCGGGCTACGGACGGCAGTGCCGGA 31440
          A  G  R  P  D  P  L  G  T  P  A  P  G  Y  G  R  Q  C  R  T
      .     .     .     .     .     .     .     .     .     .     .
31441 CGCGGGCGGCGGAACAGGACGAGGCCGGGCGGGAGTTCTGGCGCCGCGAACTGTCCGGCG 31500
          R  A  A  E  Q  D  E  A  G  R  E  F  W  R  R  E  L  S  G  A
      .     .     .     .     .     .     .     .     .     .     .
31501 CGCCACCCCGCACGACCGTCTTCCGGGGCACCGGCCGGCCCGCCGGACCGCCCGCCCGCG 31560
          P  P  R  T  T  V  F  R  G  T  G  R  P  A  G  P  P  A  R  A
      .     .     .     .     .     .     .     .     .     .     .
31561 CCACCGTCCACTACGGCACCGACGATCCGGCCCCGACCGCGGACTTCTGCCGCGAGCACG 31620
          T  V  H  Y  G  T  D  D  P  A  P  T  A  D  F  C  R  E  H  A
      .     .     .     .     .     .     .     .     .     .     .
31621 CCGTCACCGGCTACGTGCTGCTGCTCGCGGCCCTCGCCTGCCTGGTCGCCCGGTACACCG 31680
          V  T  G  Y  V  L  L  L  A  A  L  A  C  L  V  A  R  Y  T  G
      .     .     .     .     .     .     .     .     .     .     .
31681 GCCGGACGGACGTGGTGATCGGCTCACCCGTCGGACTGCGCGAGGACCCCGAAGGGCTCG 31740
          R  T  D  V  V  I  G  S  P  V  G  L  R  E  D  P  E  G  L  A
      .     .     .     .     .     .     .     .     .     .     .
31741 CCACCGTCGGCCCGATGCTCAACCTGCTGCCGCTGCGCCTCCGGCTGCACGGCGACCCCG 31800
          T  V  G  P  M  L  N  L  L  P  L  R  L  R  L  H  G  D  P  G
      .     .     .     .     .     .     .     .     .     .     .
31801 GCTTCGGCGAGGTCCTGGCCCGCACCCGGGAGACGCTGCTCGGCGCGCTGGAGCACCGCA 31860
          F  G  E  V  L  A  R  T  R  E  T  L  L  G  A  L  E  H  R  T
      .     .     .     .     .     .     .     .     .     .     .
31861 CCACACCGTTCGAGGACATCGTCGACGCGGTGGGCGCCGACCGGGACCCGGACGTCAGCC 31920
          T  P  F  E  D  I  V  D  A  V  G  A  D  R  D  P  D  V  S  P
      .     .     .     .     .     .     .     .     .     .     .
31921 CCCTCTTCCAGATCCTCTTCGCCCACGAACGCCCCCCGGCCCCACCCGCGTTACCGGGCG 31980
          L  F  Q  I  L  F  A  H  E  R  P  P  A  P  P  A  L  P  G  V
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31981  TCCGTGCCCGCGTCGTACCCGTCCCCGCTCCGGCCGCCAAGTACGAGCTCGCCGTCACCG  32040
         R  A  R  V  V  P  V  P  A  P  A  A  K  Y  E  L  A  V  T  A

32041  CCACCGAGACGCCCGACGGGCTCCGGCTGATCGTCGAGGCGGAGCACGGACACGGGGAAC  32100
         T  E  T  P  D  G  L  R  L  I  V  E  A  E  H  G  H  G  E  P

32101  CGGCCGAACTCGCCGCCTTCGCCCGCCACTTCGGCGTCCTGCTGGCCGCCGGGGTCCGCG  32160
         A  E  L  A  A  F  A  R  H  F  G  V  L  L  A  A  G  V  R  A

32161  CGCCGGACACACCGCTGAGCCGCCTGCCGCTGCTCACCGACGAGGAGCGGCGCCGGCTCA  32220
         P  D  T  P  L  S  R  L  P  L  L  T  D  E  E  R  R  R  L  T

32221  CCGACACCACGGCCCCCCGCACCGCGCCGGAGGCCCCCTACCGCCCCCTGCACCGGCTGG  32280
         D  T  T  A  P  R  T  A  P  E  A  P  Y  R  P  L  H  R  L  V

32281  TCGAGGAGTCCGCCGCCCGCCGGCCCGACGCCCTGGCGGTCGTCGGCGGCACGCGTCACC  32340
         E  E  S  A  A  R  R  P  D  A  L  A  V  V  G  G  T  R  H  L

32341  TCAGCTACCGGGAGCTGAACTGCCGCGCCAACCGGCGTGCCGCCTGGCTGCGCCGCGCTG  32400
         S  Y  R  E  L  N  C  R  A  N  R  R  A  A  W  L  R  R  A  G

32401  GCATCGGCACCGAGGACGTGGTCGGCGTCCGGCTGGAACGCGGCCCGGAACTCCTCGTCT  32460
         I  G  T  E  D  V  V  G  V  R  L  E  R  G  P  E  L  L  V  S

32461  CGCTCCTCGCCGTCCTCAAGGCCGGCGCCGCCTACCTGCCCGTCGACCCGGCGCTGCCCG  32520
         L  L  A  V  L  K  A  G  A  A  Y  L  P  V  D  P  A  L  P  A

32521  CCGAGCGGGTACGGCTGATGCTCGACGACGCCCGGGCCGCGCTGCTGCTCACCGAGACCG  32580
         E  R  V  R  L  M  L  D  D  A  R  A  A  L  L  L  T  E  T  A

32581  CGCTCGGCACCCCGCCGGCCCCGGCCGGCACCCCCGTGCACCACGTGGACGGACCGCCAC  32640
         L  G  T  P  P  A  P  A  G  T  P  V  H  H  V  D  G  P  P  P

32641  CGCCGACCCGGCCCGGGGACGACGCCGACCACACCGGCCCCGACCTGCCCACCAGCCTCG  32700
         P  T  R  P  G  D  D  A  D  H  T  G  P  D  L  P  T  S  L  A

32701  CCTACCTCCTCTACACCTCCGGGTCGACGGGCCGGCCCAAGGCCGTGGCCCTCCAGCACG  32760
         Y  L  L  Y  T  S  G  S  T  G  R  P  K  A  V  A  L  Q  H  D

32761  ACAGCGCCGCGGCGTTCCTGCGCTGGGCGGGCCGCGCCTTCGACGGCGGGGAGCTGGCCG  32820
         S  A  A  A  F  L  R  W  A  G  R  A  F  D  G  G  E  L  A  A

32821  CCGTCCTGGCCACCACCTCCGCCGGCTTCGACCTGTCGGTCTTCGAGCTGTTCGCCCCCC  32880
         V  L  A  T  T  S  A  G  F  D  L  S  V  F  E  L  F  A  P  L

32881  TGGCCCACGGCGGCACCGTCGTCCTCGCCGACAGCGCCCTGCACGTGCCCGCCCTGCCCT  32940
         A  H  G  G  T  V  V  L  A  D  S  A  L  H  V  P  A  L  P  W

32941  GGGCGCCCGCGGCGACGCTCCTGAACACCGTGCCCTCCGCGGCCGCCGCCCTGCTGGACG  33000
         A  P  A  A  T  L  L  N  T  V  P  S  A  A  A  A  L  L  D  A

33001  CCGACGGCCTGCCCGACGGTCTGACGGCCGTCAACCTGGCGGGCGAGCCCCTGACCGCGG  33060
         D  G  L  P  D  G  L  T  A  V  N  L  A  G  E  P  L  T  A  E

33061  AGCTGGTCGCCCGGCTGCACGCCCGCCTGCCGAAGGCCGCCGTCCGCAACCTCTACGGCC  33120
         L  V  A  R  L  H  A  R  L  P  K  A  A  V  R  N  L  Y  G  P

33121  CCTCGGAGGCCACCACCTACGCCACCGCGGCCCTCGTGCCCGCGGGCGGCACCGAGGCGC  33180
         S  E  A  T  T  Y  A  T  A  A  L  V  P  A  G  G  T  E  A  P

33181  CGGCCATCGGCCGGGCGCTCGGCGCGGCCCGCGTGTGGACCGCCGACGACCGGCAGCGCC  33240
         A  I  G  R  A  L  G  A  A  R  V  W  T  A  D  D  R  Q  R  P

33241  CCCTCCCCGGCGCGGTCGTCGGTGAACTCCTCATCGGCGGTACGGCCCCGGCCCGCGGCT  33300
         L  P  G  A  V  V  G  E  L  L  I  G  G  T  A  P  A  R  G  Y

33301  ACCTCGGCCGGCCGGGACCGACCGCCGACGCCTTCCGGCCCGATCCGACGGGACCGCCCG  33360
         L  G  R  P  G  P  T  A  D  A  F  R  P  D  P  T  G  P  P  G

33361  GCTCCCGGCTCTACCGCACCGGGGACCTGGCCGTACGCCGCCCCGACGGCCGGTTCGTGT  33420
         S  R  L  Y  R  T  G  D  L  A  V  R  R  P  D  G  R  F  V  F

33421  TCCTCGGCCGCAAGGACGAGCAGATCAAACTCCGCGGGGTGCGCATCGAACCGGGCGAGG  33480
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          L  G  R  K  D  E  Q  I  K  L  R  G  V  R  I  E  P  G  E  V
33481 TGGAAGCCGCTCTCCGCCAGTGCGCGCCGGTCGCCGCGGCCGCCGTCGTGCTCGCCGGGA 33540
          E  A  A  L  R  Q  C  A  P  V  A  A  A  A  V  V  L  A  G  T
33541 CCACCGCGGAGAACCACCGCCTCGTCGGCTTCGTCACCCCTTCGCCCGGCGCCCGCGTCG 33600
          T  A  E  N  H  R  L  V  G  F  V  T  P  S  P  G  A  R  V  D
33601 ACCCCGAGCGCACCCTCGCCGCGCTGCGTTCGCGCCTGCCCGCCGCCCTCGTGCCCGCCG 33660
          P  E  R  T  L  A  A  L  R  S  R  L  P  A  A  L  V  P  A  A
33661 CGCTGGTGGTGTGCGACGCCCTGCCGCTGACCGCCAACGGGAAGACCGACCGGGCCGCCC 33720
          L  V  V  C  D  A  L  P  L  T  A  N  G  K  T  D  R  A  A  L
33721 TCGCCCGGCGGGCGCGCGGACACCGGCCGGACCACGGCGCGTACGCCCCGCCCCGCACCC 33780
          A  R  R  A  R  G  H  R  P  D  H  G  A  Y  A  P  P  R  T  R
33781 GCGTCGAGAAGGCGGTCGCCGCGATCTGGCGCGAGGTGCTCGGGACCGAACGGGTGGGGA 33840
          V  E  K  A  V  A  A  I  W  R  E  V  L  G  T  E  R  V  G  I
33841 TCCACCAGGGGTTCTTCGACGCGGGCGGCACCTCCCTGTCGCTGCTGCGCCTTCACCACC 33900
          H  Q  G  F  F  D  A  G  G  T  S  L  S  L  L  R  L  H  H  R
33901 GGCTGGTCGCGTCCGTCCATCCCGGCCTCCGGCTCGCCGACGTCTTCCGGCTGCCGACCG 33960
          L  V  A  S  V  H  P  G  L  R  L  A  D  V  F  R  L  P  T  V
33961 TCGCCGCGCTCGCCGCGTTCGTGGACGGGCAGGAGGACGCGCGCGAGACGGCCGTCGGCG 34020
          A  A  L  A  A  F  V  D  G  Q  E  D  A  R  E  T  A  V  G  D
34021 ACGCGGCCCTCCGGGCCGGCCGGCGCCGCGCCGCGGTGGCCGCGCGCCGCAGGAAAGGCG 34080
          A  A  L  R  A  G  R  R  R  A  A  V  A  A  R  R  R  K  G  G
34081 GCGGACGATGAGCCATGCCGACGCGGGCGACGGGCTCGACGCGGCTGACACGACTGACGC 34140
                M  S  H  A  D  A  G  D  G  L  D  A  A  D  T  T  D  A   (orf24)
          G  R  *
34141 GGCCGACGGGATCGCCGTGATCTCGCTGGGCGGACGCTTCCCCGGAGCGGACCGGGTGGA 34200
          A  D  G  I  A  V  I  S  L  G  G  R  F  P  G  A  D  R  V  D
34201 CCGCCTCTGGACGAACCTGCTCGACCGCGAGGACGCCATCAGCCACTTCACCGCCGACGA 34260
          R  L  W  T  N  L  L  D  R  E  D  A  I  S  H  F  T  A  D  E
34261 ACGCCTCGCCCGGGGCCGCGACCCCGAACTGGTGCGCCACCCGCGGTTCGTCGGCGCGGA 34320
          R  L  A  R  G  R  D  P  E  L  V  R  H  P  R  F  V  G  A  E
34321 AGGCGTCCTCGGCGACGTCTCCCTCTTCGACGCCGAGTTCTTCGGCTGCTCGCCGCGCGA 34380
          G  V  L  G  D  V  S  L  F  D  A  E  F  F  G  C  S  P  R  E
34381 GGCCGAAGTCATGGACCCGCAGCACCGGCTCTGCCTGGAGGAGGCGTGGCACGTCTTCGA 34440
          A  E  V  M  D  P  Q  H  R  L  C  L  E  E  A  W  H  V  F  D
34441 CACCGCCGGCTACGACCCGGCGGCGACGGGCACCGCGGTCGGGGTGTTCCTCTCCGCGAG 34500
          T  A  G  Y  D  P  A  A  T  G  T  A  V  G  V  F  L  S  A  S
34501 CCTCAGCTCGTACCTGATCCGCAACGTCCTGCCCGGCGGCGCGGCACAGCGCCTGCTCGG 34560
          L  S  S  Y  L  I  R  N  V  L  P  G  G  A  A  Q  R  L  L  G
34561 CGGCTTCCCGCTGCTGATCCACAACGACAAGGACTTTCTGGCCACCACCGTGTCCCACAA 34620
          G  F  P  L  L  I  H  N  D  K  D  F  L  A  T  T  V  S  H  K
34621 ACTGGGCCTCACCGGGCCGAGTTACGCCGTCGGCTCGGCCTGCTCGTCCTCCCTCGTCGC 34680
          L  G  L  T  G  P  S  Y  A  V  G  S  A  C  S  S  S  L  V  A
34681 GGTGCACCTGGCCTGCCAGAGCCTGCTCACCGAGGAATGCGACATGGCGCTGGCCGGCGG 34740
          V  H  L  A  C  Q  S  L  L  T  E  E  C  D  M  A  L  A  G  G
34741 GGTCTCGCTCCAAGTGCCGCAGGGCCAGGGGTACGTGCACGCCGACGACGGCATCTACTC 34800
          V  S  L  Q  V  P  Q  G  Q  G  Y  V  H  A  D  D  G  I  Y  S
34801 ACCCGACGGGCGCTGCGCCCCCTTCGACGCCGGCGCGGCGGGCACGGTGGGCGGCAGCGG 34860
          P  D  G  R  C  A  P  F  D  A  G  A  A  G  T  V  G  G  S  G
34861 CGTGGGCCTCGTCCTGCTCAAGCGGCTCGCCGACGCCGTGCGCGACGGGGACCGCGTCCA 34920
          V  G  L  V  L  L  K  R  L  A  D  A  V  R  D  G  D  R  V  H
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34921  CGCGGTGATCCTCGGCTCGGCGGTGAACAACGACGGCGCCGACAAGGTCGGTTACACGGC  34980
         A  V  I  L  G  S  A  V  N  N  D  G  A  D  K  V  G  Y  T  A

34981  GCCCGGCGTCACCGGCCAGAGCGCCGTCGTCGCCGAGGCCCTGGCGGTGGCCGGGATCTC  35040
         P  G  V  T  G  Q  S  A  V  V  A  E  A  L  A  V  A  G  I  S

35041  CGCCGCGACCGTCGGCGTCCTGGAGGCGCACGGCACCGGCACCCGGCTGGGCGATCCCGT  35100
         A  A  T  V  G  V  L  E  A  H  G  T  G  T  R  L  G  D  P  V

35101  CGAAGTGGCCGCGCTCACCCGGGCGTTCCGCGCCCACACGGACCGCAGCGGCTTCTGCGC  35160
         E  V  A  A  L  T  R  A  F  R  A  H  T  D  R  S  G  F  C  A

35161  GCTGGGCTCGGTGAAGGCCAACGTGGGCCACCTGGACGCGGCGGCGGGCGTCACCGGGCT  35220
         L  G  S  V  K  A  N  V  G  H  L  D  A  A  A  G  V  T  G  L

35221  GATCAAGGCCGTGCTGGCGGTCCGCGAGGGCGTCATCCCCGGCACCCCGCACTACCGTTC  35280
         I  K  A  V  L  A  V  R  E  G  V  I  P  G  T  P  H  Y  R  S

35281  GCCCAACCCCGCCATCGACTTCGCCACCACACCCTTCTACGTCACCGCCGACACCCTCGC  35340
         P  N  P  A  I  D  F  A  T  T  P  F  Y  V  T  A  D  T  L  A

35341  CTGGCCGGAGGCGGACCACCCCCGCCGGGCCGGCGTCAGCTCCTTCGGCATCGGGGGCAC  35400
         W  P  E  A  D  H  P  R  R  A  G  V  S  S  F  G  I  G  G  T

35401  CAACGCCCACGTGATCCTGGAACAGGCCCCGCCGGCCGCCCCCCGCGCGGACCGGACCGC  35460
         N  A  H  V  I  L  E  Q  A  P  P  A  A  P  R  A  D  R  T  A

35461  CGGGGTGCCCATGCCGTTGGTGGTGTCCGCCCGCACCCGCGAAGCACTGGCGGAGGCCGT  35520
         G  V  P  M  P  L  V  V  S  A  R  T  R  E  A  L  A  E  A  V

35521  CCGGGACCTGGCGGCGTGGTCGGCCCCGGAGCCGGGGACCCGGCTCGCCGATCTCGCCGC  35580
         R  D  L  A  A  W  S  A  P  E  P  G  T  R  L  A  D  L  A  A

35581  CACGCTGGCCGGGCGCCGGGCCTTCCCGTACCGCGCCGCCGTCGTGTGCCACGACCTGCC  35640
         T  L  A  G  R  R  A  F  P  Y  R  A  A  V  V  C  H  D  L  P

35641  CGAGGCCGCGCGCCTGCTGGGCGGCGCGCGCGGCGAGACCGCGCTCCCCGGCAGGGAGGC  35700
         E  A  A  R  L  L  G  G  A  R  G  E  T  A  L  P  G  R  E  A

35701  CGTGTTCCTCTTCCCCGGGCAGGGCACCCTCCCGCCGGACACCGGGCGCGGCCTGTACGC  35760
         V  F  L  F  P  G  Q  G  T  L  P  P  D  T  G  R  G  L  Y  A

35761  GGACGTGCCGGCGTTCCGCGCCCACTTCGACGCCTGTGCCGAAGGGTTCGCCCCGCTCGG  35820
         D  V  P  A  F  R  A  H  F  D  A  C  A  E  G  F  A  P  L  G

35821  CACCGACCTCCACGCCGCGCTCGGGGCCCCGGCCGACGACACCAGGGCCGCGCAACCCGC  35880
         T  D  L  H  A  A  L  G  A  P  A  D  D  T  R  A  A  Q  P  A

35881  CCTCTTCGCCGTCGAGTACGCCCTCGCCCGCACCCTGATGGACTGGGGTGTGCGCCCGGC  35940
         L  F  A  V  E  Y  A  L  A  R  T  L  M  D  W  G  V  R  P  A

35941  CGCGATGCTCGGGCACAGCCTCGGCGAGTACGTCGCGGCGACGCTGGCCGGGGTGCTGTC  36000
         A  M  L  G  H  S  L  G  E  Y  V  A  A  T  L  A  G  V  L  S

36001  CCTGCCGGACGCGCTGACGCTCGTCCGGGCCCGGGCGGAAGCGCAGCACACCATGCCGCC  36060
         L  P  D  A  L  T  L  V  R  A  R  A  E  A  Q  H  T  M  P  P

36061  CGGCCGCATGCTCGCGGTCCCGCTCACGCCGGACGACCTGCGCCCGCTGCTGCCCCCGGA  36120
         G  R  M  L  A  V  P  L  T  P  D  D  L  R  P  L  L  P  P  E

36121  GGTGGAGTTCAGCGCCTTCAACGCCCCCGGCCGCTGCGTCGTCGGCGGGCCCCCGGAGCC  36180
         V  E  F  S  A  F  N  A  P  G  R  C  V  V  G  G  P  P  E  P

36181  GGTGGCGGAGCTGCGCGCCCGGCTGGCGCGGCGCGGAGTGCCGGCCGCCGAACTGGCCAC  36240
         V  A  E  L  R  A  R  L  A  R  R  G  V  P  A  A  E  L  A  T

36241  CGCGCACGCCTTCCACTCGGCGGCCGTCGAACCGCTGCTGGACGGCTTCCGGGGCGTGCT  36300
         A  H  A  F  H  S  A  A  V  E  P  L  L  D  G  F  R  G  V  L

36301  GGAAGGCGTCCGACTGCGGCCGCCCCGGCTGCGGTACGTGTCCTCCCTCACCGGCGACTG  36360
         E  G  V  R  L  R  P  P  R  L  R  Y  V  S  S  L  T  G  D  W

36361  GGCCGACGCCGCGGTCACCACCCCCGCGTACTGGCTCGCCCACCTGCGCCGGCCCGTCCG  36420
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[redacted] [redacted]

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          A  D  A  A  V  T  T  P  A  Y  W  L  A  H  L  R  R  P  V  R
          .     .     .     .     .     .     .     .     .     .
36421  CTTCGCCGACGGCCTGCGGCGCTGCCTGGACCTCGGCCCCGTCGCCCTGGTCGAGACCGG  36480
          F  A  D  G  L  R  R  C  L  D  L  G  P  V  A  L  V  E  T  G
          .     .     .     .     .     .     .     .     .     .
36481  GCCGCGGGCCGGACTGACCGGCCTGGCCCGCCGCGCCGCGGGCCCCGGCGAGCCCCCTTA  36540
          P  R  A  G  L  T  G  L  A  R  R  A  A  G  P  G  E  P  P  Y
          .     .     .     .     .     .     .     .     .     .
36541  CACCGTCCGCTGCCTGGCCGCCCCCGACGAGGCGGCTTCGCTGACCCACGCGGTCGCCGT  36600
          T  V  R  C  L  A  A  P  D  E  A  A  S  L  T  H  A  V  A  V
          .     .     .     .     .     .     .     .     .     .
36601  ACTCTGGCGCTCGGGCTGCGCCGTCGACTGGACGGCGTTCCACCGCCCCGGGCGCCCCCG  36660
          L  W  R  S  G  C  A  V  D  W  T  A  F  H  R  P  G  R  P  R
          .     .     .     .     .     .     .     .     .     .
36661  CCGCACCACCGTGCCCGGCTACCCCTTCCAACGGGTACGGCACTGGATCGACGCGCCGGA  36720
          R  T  T  V  P  G  Y  P  F  Q  R  V  R  H  W  I  D  A  P  D
          .     .     .     .     .     .     .     .     .     .
36721  CGAGTCCGAACCCACGGACCTCGCCACCGCCCTGCGCGCGGAGTTGCGGACGGACGGCGA  36780
          E  S  E  P  T  D  L  A  T  A  L  R  A  E  L  R  T  D  G  D
          .     .     .     .     .     .     .     .     .     .
36781  TCCGCCGCTCGCCGTCGATCAGCGGCCCGGACTGCGCACGGGGCTGAACCGGCTGTGCGC  36840
          P  P  L  A  V  D  Q  R  P  G  L  R  T  G  L  N  R  L  C  A
          .     .     .     .     .     .     .     .     .     .
36841  CGCCCTGGCCCGCGACTACCTGGCCACCGGCGTCGAAGCGAGCGGGGTCCTGCCCGGATT  36900
          A  L  A  R  D  Y  L  A  T  G  V  E  A  S  G  V  L  P  G  F
          .     .     .     .     .     .     .     .     .     .
36901  CCACCGCTTCCTGGACTACCTGCGCACCCTGGCCGCCTCCGCACCGGCCGCGGACGACGC  36960
          H  R  F  L  D  Y  L  R  T  L  A  A  S  A  P  A  A  D  D  A
          .     .     .     .     .     .     .     .     .     .
36961  GGGGACGATCGCCGCGGAGATCACCGCGGCCCACCCGTCCTTCTCCGGGCTCGTCGACCT  37020
          G  T  I  A  A  E  I  T  A  A  H  P  S  F  S  G  L  V  D  L
          .     .     .     .     .     .     .     .     .     .
37021  GCTCCGGCACTGCGCCCAGGGCTATCCGCGCGCCCTGTCCACCCCCGGAGCCGCACTGGA  37080
          L  R  H  C  A  Q  G  Y  P  R  A  L  S  T  P  G  A  A  L  D
          .     .     .     .     .     .     .     .     .     .
37081  CGTCCTCTATCCGGCCGGCAGCGGCGACCTCCTGCGCCGCACCCTGGGCGAGGGCACCGC  37140
          V  L  Y  P  A  G  S  G  D  L  L  R  R  T  L  G  E  G  T  A
          .     .     .     .     .     .     .     .     .     .
37141  CGACCACCGCGCCACCGGCCGCCTCACCCGGCTGGCCGGCTCCCTGCTCGACCGGCTCGC  37200
          D  H  R  A  T  G  R  L  T  R  L  A  G  S  L  L  D  R  L  A
          .     .     .     .     .     .     .     .     .     .
37201  GGCCGACCGCGAACCCGGCCGCCCGCTGCGCGTCCTGGAGGCCGGAGCGGGCGCGGGCAG  37260
          A  D  R  E  P  G  R  P  L  R  V  L  E  A  G  A  G  A  G  S
          .     .     .     .     .     .     .     .     .     .
37261  CCTCACCCAGGCCCTGGTCACCCGGGCCCCCGGCCGGCTCGACTACCACGCCACCGACAT  37320
          L  T  Q  A  L  V  T  R  A  P  G  R  L  D  Y  H  A  T  D  I
          .     .     .     .     .     .     .     .     .     .
37321  CTCCCGGCACTTCGTGACCGCACTCGGCCGGGAGGCCGCCCGGCGCGGCCTGGACTTCGT  37380
          S  R  H  F  V  T  A  L  G  R  E  A  A  R  R  G  L  D  F  V
          .     .     .     .     .     .     .     .     .     .
37381  CCGCGCACGCGTCCTCGACATCGCCCGCGACCCAGGCGAACAGGGCTTCGCCGGCGAGCG  37440
          R  A  R  V  L  D  I  A  R  D  P  G  E  Q  G  F  A  G  E  R
          .     .     .     .     .     .     .     .     .     .
37441  GTTCGACGTCGTCTGCGGCCTCGACGTGGTCCACGCCACCCCCGACCTGCGCACCACGCT  37500
          F  D  V  V  C  G  L  D  V  V  H  A  T  P  D  L  R  T  T  L
          .     .     .     .     .     .     .     .     .     .
37501  CGGCCATCTGCGCTCCCTGATGGCACCGGACGGCACCCTCGCGCTGATCGAGACCACCGC  37560
          G  H  L  R  S  L  M  A  P  D  G  T  L  A  L  I  E  T  T  A
          .     .     .     .     .     .     .     .     .     .
37561  CGACGACCCCTGGCTGACGATGATCTGGGGCCTGACGGACGGCTGGTGGCACCACACCGA  37620
          D  D  P  W  L  T  M  I  W  G  L  T  D  G  W  W  H  H  T  D
          .     .     .     .     .     .     .     .     .     .
37621  CCGGCGCACCCACGGCCCGCTGCTCGACGCCGCCGGCTGGCGCGCCCTCCTGGCCGGCGA  37680
          R  R  T  H  G  P  L  L  D  A  A  G  W  R  A  L  L  A  G  E
          .     .     .     .     .     .     .     .     .     .
37681  GGACTTCGCCACGGCCGATGTGATCGTGCCGCCCGACGGCCCCCAGGACGCGGCCCTGCT  37740
          D  F  A  T  A  D  V  I  V  P  P  D  G  P  Q  D  A  A  L  L
          .     .     .     .     .     .     .     .     .     .
37741  GCTCGCCCGGCAGACCCCCCGGCCGGCGGCGGCCGCACCGTCCGTCGGCAAGCGGGACGT  37800
          L  A  R  Q  T  P  R  P  A  A  A  A  P  S  V  G  K  R  D  V
          .     .     .     .     .     .     .     .     .     .
37801  CGGCACGTGGTGCTACGCCCGCGGCTGGCGGCACGCCGCGCCCGCCGACCCCGCCCCGCT  37860
          G  T  W  C  Y  A  R  G  W  R  H  A  A  P  A  D  P  A  P  L
          .     .     .     .     .     .     .     .     .     .
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37861 GACGGGCGGCTGCCTGCTGCTGGGCGACGGGGACACGGCGAAGGCCGTCGCGAGCCGGCT 37920
T G G C L L L G D G D T A K A V A S R L

37921 GGAGGCCCTCGGCGTGCCCGTCACCACCGTCGGCGGCGGCCGACCGCCGGGCCCCGAGCG 37980
E A L G V P V T T V G G G R P P G P E R

37981 GTACCGGGAACTCGTCGGCCCCGCCACCCGCCTGGCCGTCGACCTGTGGCCGCTGCGCGA 38040
Y R E L V G P A T R L A V D L W P L R D

38041 CGCGTCCCACCGCGGCCGCGCCGCCGGCGCCGCCGGCGTACGGACCGCCCAGGACGCCGC 38100
A S H R G R A A G A A G V R T A Q D A A

38101 GCTGCACAACCTGCTCCACCTCGCCCGGGCCTTCGGCGCGCTGGAGGAGCGCCACCCCGC 38160
L H N L L H L A R A F G A L E E R H P A

38161 CCGCGTCGTGACCGTGACCACCGGTGCCCACGACGTGCTCGGCGACGACCTCGCCCACCC 38220
R V V T V T T G A H D V L G D D L A H P

38221 CGAGCACGCCACCGTCCCGGCCGCGGCCAAGGTGATCCCCCGGGAGTACCCGTGGATCGC 38280
E H A T V P A A A K V I P R E Y P W I A

38281 CTGCACCGCCCTGGACGTGGAGCCGGGCCTGGACGCCGAGCGGCTGGCGGACCTGATCGT 38340
C T A L D V E P G L D A E R L A D L I V

38341 CCGGGAACTCGGCGCGGCGCGCGAGACCACCGTCACCGCCTGCCGCGGCCGACGCCGCTT 38400
R E L G A A R E T T V T A C R G R R R F

38401 CACCCCCTGCCCCGTCCGGCAGCCCCTCCCCGCCGCACCGGAACGCCCGGCGGTCCGGCC 38460
T P C P V R Q P L P A A P E R P A V R P

38461 CGGCGGCGTCTACCTCGTCTGCGGCGGCCTCGGCGGCATCGGCCTCCACCTCGCCGAGTA 38520
G G V Y L V C G G L G G I G L H L A E Y

38521 CCTGGGCCGCGCCCGCACCACCGTCGTCCTCACCCACCGGCGGCCCTTTCCCGCCCCCGG 38580
L G R A R T T V V L T H R R P F P A P G

38581 CGCGTGGGACGGGCTGCCCGCGGGACACCCGGAGGCGGCCGTCGTCCGGCGGCTGCGCTC 38640
A W D G L P A G H P E A A V V R R L R S

38641 CCTCGCCGCCACCGGCGCCACGGTCGTCGTCCGCCGGGCCGACCTCACCGACCACGACGC 38700
L A A T G A T V V V R R A D L T D H D A

38701 GATGCGCGCCCTCGCGGACGAGGTGGAACAGGCCCACGGCCCCGTCCGGGGGGTGGTGCA 38760
M R A L A D E V E Q A H G P V R G V V H

38761 CGCGGCCGGGGTGCCCGACACCGCCGGCATGATCCAGCGTCGCGACCGAGCCGGCACGGA 38820
A A G V P D T A G M I Q R R D R A G T D

38821 CGCCGCCCTCGCCGCCAAACTGACCGGCACCCTCGTCCTGGACGAGGTGTTCGCCCACCG 38880
A A L A A K L T G T L V L D E V F A H R

38881 CGACCTCGACTTCCTCGTCCTGTGCTCCTCGATCGGCACCGTGCTGCACAAGCTGAAGTT 38940
D L D F L V L C S S I G T V L H K L K F

38941 CGGCGAGGTCGGCTACGTGGCGGGCAACGAGTTCCTCGACGCCTATGCCGCCCACCGCGC 39000
G E V G Y V A G N E F L D A Y A A H R A

39001 GGCCCGCCGCCCCGGCAGAACCCTGTCGATCGCCTGGACCGACTGGCGGGAGTCGGGCAT 39060
A R R P G R T L S I A W T D W R E S G M

39061 GTGGGCCGCCGCCCAGCGCCGTCTGACCGAGCGCTACGGCACCGGCGCCGACCTGCCCGT 39120
W A A A Q R R L T E R Y G T G A D L P V

39121 ACCGCCCGGGGGCGACCTGCTCGGCGCGATCAGCCCCGAGGAGGGCGTCGACGTCTTCGC 39180
P P G G D L L G A I S P E E G V D V F A

39181 CCGGCTGCTCGCCGCCGACACCGGCCCGAACGTCATCGTGTCGGCCCAGGACCTCGACGA 39240
R L L A A D T G P N V I V S A Q D L D E

39241 ACTCCTCGCGCGGCACGCGGCGTACACCACCGACGACCACCTCGCCGCCCTCGGCGACCT 39300
L L A R H A A Y T T D D H L A A L G D L

39301 GAGGATCGCCGCCGCCCGGGACCGCTCCGCGCCCGCCGCGCCGTACGCGGCCCCCCACAC 39360
R I A A A R D R S A P A A P Y A A P H T

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39361  GCCCGCCCAGCGGCGGATCGCCGGCTGGTACCGCGACCTGCTCGGCGTCGAACACGTCGG   39420
         P  A  Q  R  R  I  A  G  W  Y  R  D  L  L  G  V  E  H  V  G

39421  CCTCGACGACGACTTCTTCGCGCTCGGCGGGGACTCGCTGCTCGCCCTGCGCCTGCTGTC   39480
         L  D  D  D  F  F  A  L  G  G  D  S  L  L  A  L  R  L  L  S

39481  GCAGCTGCGGGACGCCTACGGGGTGGAGATCTCCGTCGCCCGCATGTTCGACGAGCCCAC   39540
         Q  L  R  D  A  Y  G  V  E  I  S  V  A  R  M  F  D  E  P  T

39541  GGTGGCGGCGCTGGCCGCCGCCACCGGCCCGCCGCCGGAAGAGACGCCCGGCCAGGAAGA   39600
         V  A  A  L  A  A  A  T  G  P  P  P  E  E  T  P  G  Q  E  E

39601  GGTGGTGCTGTGACCACGCCCCGCATCACCGACCTGCTCACCGAGCTCCGCGGCCGGCAG   39660
         V  V  L  *
                  M  T  T  P  R  I  T  D  L  L  T  E  L  R  G  R  Q    (orf23)

39661  GTGACCCTCACGGCCGACGGGGACCGGCTGCACTGCCGCGCGCCCCGGGGCGCGCTCACC   39720
         V  T  L  T  A  D  G  D  R  L  H  C  R  A  P  R  G  A  L  T

39721  GACGAGCTCCTCGCCACCATCCGCGCCCGCCGCGACGAACTCCTCGCCCACCTGCGCGCC   39780
         D  E  L  L  A  T  I  R  A  R  R  D  E  L  L  A  H  L  R  A

39781  GACCGCCGCATCCCGCGCCACGACGGGCCCGCGCCGCTGTCCTTCGCCCAGGAACGGCTC   39840
         D  R  R  I  P  R  H  D  G  P  A  P  L  S  F  A  Q  E  R  L

39841  TGGCTCCTCCACCAGTTCCACCCGCACGACAGCGCCTACAACATCCCCCTGCACATCGCC   39900
         W  L  L  H  Q  F  H  P  H  D  S  A  Y  N  I  P  L  H  I  A

39901  CTGCGCGGGCCCCTGAACCCGGCCGCCCTGCGCGCCGCCCTGGCCGAGGTGGTACGGCGG   39960
         L  R  G  P  L  N  P  A  A  L  R  A  A  L  A  E  V  V  R  R

39961  CACGACGTCCTGCGCACCCGGTACGCCATCAGCCGCGGCCTGCCCCGGCCCGTCGTCGAA   40020
         H  D  V  L  R  T  R  Y  A  I  S  R  G  L  P  R  P  V  V  E

40021  CCGGCCCACACGCCGCCGCTGCCCCTGACCGACCTGACCGGGCTCCCCGCACACCACCGG   40080
         P  A  H  T  P  P  L  P  L  T  D  L  T  G  L  P  A  H  H  R

40081  GACGCCGAACTCGCCCGGCTGGCCGCCCAGGAGGCCAGGCGGCCCTTCGACCTCGCCCAG   40140
         D  A  E  L  A  R  L  A  A  Q  E  A  R  R  P  F  D  L  A  Q

40141  GGCCCGGTGCTGCGGGCCCGGCTCCTCCGAACGGCCCCCGAGGAGCACCGGCTGCTGCTG   40200
         G  P  V  L  R  A  R  L  L  R  T  A  P  E  E  H  R  L  L  L

40201  ACCCGCCATCACATCGCCAGCGACGGCTGGTCGCTCGACATCCTGCTCCGCGAACTGGGC   40260
         T  R  H  H  I  A  S  D  G  W  S  L  D  I  L  L  R  E  L  G

40261  ACGTTCTACCGGGCAGGGCGGGACGGCACACCCGCCGGCCTCGACGCCCTGCCGCTGCGG   40320
         T  F  Y  R  A  G  R  D  G  T  P  A  G  L  D  A  L  P  L  R

40321  TACGCCGACTTCGCCGCGTACCAGCGCGAACAGGCCGAACGGCCGGAGACGGCCGAGCGG   40380
         Y  A  D  F  A  A  Y  Q  R  E  Q  A  E  R  P  E  T  A  E  R

40381  TCGACCCGCTGGGCACGGCACCTGAGGGGCGCCCCCGCGACACTCGACGTCCTCGGGCCC   40440
         S  T  R  W  A  R  H  L  R  G  A  P  A  T  L  D  V  L  G  P

40441  CCGCCCGCCGAACCCTCCCACGCGCCGGCCGGCACCGTACGGACGGACCTTCCCGCCGCC   40500
         P  P  A  E  P  S  H  A  P  A  G  T  V  R  T  D  L  P  A  A

40501  CTCGTCACCGGCCTGCGGCAGCTGGGCGGCCGGGCCCGCACCACGCTCTTCCCGCTCCTG   40560
         L  V  T  G  L  R  Q  L  G  G  R  A  R  T  T  L  F  P  L  L

40561  CTGAGCGCCTTCGGCCTCGCCCTGGCCGGCCCGCCCGGCCCGTACGACGTCATGGTCGGC   40620
         L  S  A  F  G  L  A  L  A  G  P  P  G  P  Y  D  V  M  V  G

40621  ATCCCCGTCGCCGGCCGGCCGCGCACCGAACTGGAGCCGCTCATCGGCTGCTTCGCGACC   40680
         I  P  V  A  G  R  P  R  T  E  L  E  P  L  I  G  C  F  A  T

40681  ATCGCGCCGATGCGGCTGACGAGCGACGGGACCGAGCCGCTGACCCGGCTCGCCGCCCGC   40740
         I  A  P  M  R  L  T  S  D  G  T  E  P  L  T  R  L  A  A  R

40741  GCCCAGCAGCACGTCCAGGACGCGCTGGACGGACCCGACGTCCCCTTCGAGCGGCTCGTG   40800
         A  Q  Q  H  V  Q  D  A  L  D  G  P  D  V  P  F  E  R  L  V
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40801 CACGCGCTGCGTCCGGAGCGGGACCTCGCGGAGAACCCCCTGTTCTCGGCGTCGTTCGCC 40860
      H  A  L  R  P  E  R  D  L  A  E  N  P  L  F  S  A  S  F  A

40861 TTCCAGAACACCCCGCGGACCGCCGTGCGCCTCCCCGGCCTGGACGCCGAGGTGCTGCCC 40920
      F  Q  N  T  P  R  T  A  V  R  L  P  G  L  D  A  E  V  L  P

40921 TCGCCGCCCGTGGCCCCCAAGTTCCCGCTGGCCCTCACCGCGACGGCGCGGGCCGACGGC 40980
      S  P  P  V  A  P  K  F  P  L  A  L  T  A  T  A  R  A  D  G

40981 GGAATGGGCCTGGAGCTGGAGTTCGACCGGGACCGGATCGCCGAGCCGGTCGCGCGGGGG 41040
      G  M  G  L  E  L  E  F  D  R  D  R  I  A  E  P  V  A  R  G

41041 ATCCTCACGTCCTTCCACGCCGCCCTCGCCCGCGCGGTCGCCGACCCCGAGGCCCCGGCG 41100
      I  L  T  S  F  H  A  A  L  A  R  A  V  A  D  P  E  A  P  A

41101 GCGCCCGTACCGGCCGCCGCCGTGGACCGGCGGCCCGGGCGCGAAGGACACGAGTGCCTC 41160
      A  P  V  P  A  A  A  V  D  R  R  P  G  R  E  G  H  E  C  L

41161 CACGAGCCGGTGGCGCGGGCGGCGGCACGCCACCCCGACGCCGTCGCCGTCAGCTGCGGC 41220
      H  E  P  V  A  R  A  A  A  R  H  P  D  A  V  A  V  S  C  G

41221 GGCACCCAGCTCAGCTACGGGGCGCTCGACACCCGCGCCGAACGGCTGGCCGCGGTGCTG 41280
      G  T  Q  L  S  Y  G  A  L  D  T  R  A  E  R  L  A  A  V  L

41281 CGCGCCCACGGCGCCGGCCCCGAGCGGCTGGTGGCCCTGTGCCTGCCCACCGGCCCCGAA 41340
      R  A  H  G  A  G  P  E  R  L  V  A  L  C  L  P  T  G  P  E

41341 TGGGTCGTCGGCGCCCTCGCCATCCTCAAGTCCGGCGCCGCCTACCTGCCGCTCGACCCC 41400
      W  V  V  G  A  L  A  I  L  K  S  G  A  A  Y  L  P  L  D  P

41401 GGCGACCCGGCCGAGCGCCGCGCCTCCGTCGCCGCCGACGCGGGAGCGACGCTGATCGTC 41460
      G  D  P  A  E  R  R  A  S  V  A  A  D  A  G  A  T  L  I  V

41461 TCCGACACCGCGCTTCCCCCGCTCCACCGCGTCGACGTCACGGCCACCCTCCCGGACGGC 41520
      S  D  T  A  L  P  P  L  H  R  V  D  V  T  A  T  L  P  D  G

41521 GCCCCCGAGCCCACCGCCCGGGCCGTCCTGCCCGGCAACCTCGCCTACGCCGTCTACACC 41580
      A  P  E  P  T  A  R  A  V  L  P  G  N  L  A  Y  A  V  Y  T

41581 TCCGGCTCCACCGGCGGCCCCAAGGGCGTGCTCGTCACCCATGCCAACGTCACCGGGCTC 41640
      S  G  S  T  G  G  P  K  G  V  L  V  T  H  A  N  V  T  G  L

41641 CTGGCCGCGTGCCGTGAGGCCCTGCCCGCCCTGGACGCCCCCCGGACCTGGTCGGCGACC 41700
      L  A  A  C  R  E  A  L  P  A  L  D  A  P  R  T  W  S  A  T

41701 CACTCGCCGGCCTTCGACTTCTCCGTCTGGGAGGTCTGGGGCCCGCTGACCGCCGGCGGA 41760
      H  S  P  A  F  D  F  S  V  W  E  V  W  G  P  L  T  A  G  G

41761 CGCCTCGTCCTCGTGCCCCCGGACGTGGCCCGGGCCCCGGACGAACTGTGGGACACCCTC 41820
      R  L  V  L  V  P  P  D  V  A  R  A  P  D  E  L  W  D  T  L

41821 CGCGACGAACAGGTCGAAGTCCTCAGCCAGACCCCCAGCGCGTTCCACCACCTCCTGCCC 41880
      R  D  E  Q  V  E  V  L  S  Q  T  P  S  A  F  H  H  L  L  P

41881 ACCGCCGTGCGCCGGGCGGCCCAGGCCACCGCGCTCGAACTCGTCGTCCTGGGCGGCGAG 41940
      T  A  V  R  R  A  A  Q  A  T  A  L  E  L  V  V  L  G  G  E

41941 GCGTGCGAGCCCGCCCGTCTGACGCCTTGGTGGGACGCCCTGGGCGACCGGCGCCCGGCC 42000
      A  C  E  P  A  R  L  T  P  W  W  D  A  L  G  D  R  R  P  A

42001 GTGGTCAACATGTACGGCATCACCGAGAACACCATCCACGTCACCGTCCGCCGGATGACG 42060
      V  V  N  M  Y  G  I  T  E  N  T  I  H  V  T  V  R  R  M  T

42061 GCGGCGGACCGGTCGGGCAGTCCCGTCGGCCGGCCGCTGCCGGGGCAGCGCGCCGACCTT 42120
      A  A  D  R  S  G  S  P  V  G  R  P  L  P  G  Q  R  A  D  L

42121 CTCGACCCCCACGGCCGGCCCGTCGCGCCGGGCGGGCGGGGCGAACTGTTCGTCGGCGGC 42180
      L  D  P  H  G  R  P  V  A  P  G  G  R  G  E  L  F  V  G  G

42181 GTCGGACTGGCCCGCGGCTACCTCGGCCGGCCCGGCCTCACCGCCCGGAGCTTCCTGCCG 42240
      V  G  L  A  R  G  Y  L  G  R  P  G  L  T  A  R  S  F  L  P

42241 GACGACACCCCCGGCTGGCCGGGCGCGCGCCGCTACCGCTCCGGAGACCTGGCCCGGCTG 42300
      D  D  T  P  G  W  P  G  A  R  R  Y  R  S  G  D  L  A  R  L
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42301 CTGCCCGACGGCGGCCTGGACTACGCGGGCCGCTCCGACGCACAGGTCAAGGTCCGCGGC 42360
L P D G G L D Y A G R S D A Q V K V R G

42361 TACCGCGTCGAGCCCGCCGAGACCGAAGCCGCCGCGCTGACCCATCCCGCCGTGCGCCAC 42420
Y R V E P A E T E A A A L T H P A V R H

42421 TGCGTGGTCGTGCCACGCGGCGACGGCGACCGGCGCCATCTCGCGGCGTACGTCGTCGCC 42480
C V V V P R G D G D R R H L A A Y V V A

42481 GACACCCGCGCCTGCGACGGGCCCGGGCTCCGCACCCACCTGGCCGAGCGGCTGCCCCGC 42540
D T R A C D G P G L R T H L A E R L P R

42541 CACCTGGTGCCGGCCTCGGTGGTCTTCCTGAAGCGGATCCCGCTGACCCGCAACGGCAAG 42600
H L V P A S V V F L K R I P L T R N G K

42601 CTCGACGTGGCGGCCTTGCCCGACCCGGCCGCCCACCGCGCACCCGCCCGCGAACGCCCG 42660
L D V A A L P D P A A H R A P A R E R P

42661 CGCACCGCGACCGAACGGACCCTCACCCGGCTGCTCGCCGCCCTCCTGAAGGCGCCACCG 42720
R T A T E R T L T R L L A A L L K A P P

42721 GAGACCATCGGGACGCACGACAACCTCTTCGACCTGGGCGGCGACTCCCTGACGGTCACC 42780
E T I G T H D N L F D L G G D S L T V T

42781 CAGTTCCACTCCCGGGTGGTGGAGGAGTTCGCCGTGGACCTCCCGGTGCGCCGGGTCTAC 42840
Q F H S R V V E E F A V D L P V R R V Y

42841 CAGGCCCTCGACATCGCGACGCTCGCCGTGACCGTGGACGACTTCCGGCGCCGCGCCGAA 42900
Q A L D I A T L A V T V D D F R R R A E

42901 CGCACCGCGGTACTGCGCGCCCTCGCGGCGGCGGAGGCGATGGAACCCGGCGGTACGGCG 42960
R T A V L R A L A A A E A M E P G G T A

42961 GGGGAGTCCGGCGGTAATCCGGAGGAGTCCGCCGCTACGGCGCGGGGGCCCGCCGTCGCG 43020
G E S G G N P E E S A A T A R G P A V A

43021 GCGAACGAACCCGGCGCTGCGGCGCGTGAGTCCGGCGCCGCGCCGGTGGAGCCCGCCGTC 43080
A N E P G A A A R E S G A A P V E P A V

43081 GCAGTACAGGAGTCCGCCGCTACGAAGGGGGAGCCCGGCACCGCAGCGAATGAACTCGGC 43140
A V Q E S A A T K G E P G T A A N E L G

43141 GCTGAGGCACGGGAGCCCGGCACCGCAGCGCAGGAACCCGGCACCGACCCCCGGCCACCC 43200
A E A R E P G T A A Q E P G T D P R P P

43201 GCCGCCACACCGCAGGACCCCCGCACCACACCGCAGGAAGGACAGCCGTGCCCGCGTCCC 43260
A A T P Q D P R T T P Q E G Q P C P R P

43261 GAATGAGCCGGCCGGCCGGCATCGTCGACATCGCGCGCCGTCACGCCGAGCGCACCCCCG 43320
M S R P A G I V D I A R R H A E R T P A **(orf22)**
E *

43321 CCCGTCCCGCGTACGCGTTCCTGCCCGACGGCGAGACGGAGAGCGTCCGCTTCTCCTTCG 43380
R P A Y A F L P D G E T E S V R F S F A

43381 CCGACATCGACCGGCGGGCCCGCGCCGTGGCCGCCGTCCTCCAGGACCGCGGCCTGGCCG 43440
D I D R R A R A V A A V L Q D R G L A G

43441 GGGAGCGGGTCCTGGTCGCCTATCCCTCCGGGCCCGAGTACGTCCAGGCGTTCCTGGGCT 43500
E R V L V A Y P S G P E Y V Q A F L G C

43501 GCCTGTACGCGGGCGTGGTCGCCGTCCCCTGCGACGAGCCGCGCTCCGGCCCGAGCGCGG 43560
L Y A G V V A V P C D E P R S G P S A E

43561 AACGGCTCGCCGGGATCCGCGCCGACGCCCGCCCCGCCCTGGCCCTGACCGCCGGCGCCC 43620
R L A G I R A D A R P A L A L T A G A P

43621 CCGAGGCCGGGCTCGCCGGCCTGGCCACCCTGGACGTGGCCGGCGTCCCCGACTCCGCCG 43680
E A G L A G L A T L D V A G V P D S A A

43681 CCGGGGCCTGGACCGACCCCGTCGCGGGACCGGACGCCCTGGCCTTCCTCCAGTACACCT 43740
G A W T D P V A G P D A L A F L Q Y T S

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43741  CCGGATCGACCCGCCGCCCCCGCGGCGTCATGGTCGGCCACGGCAATCTGCTGGCCAACG  43800
         G  S  T  R  R  P  R  G  V  M  V  G  H  G  N  L  L  A  N  E

43801  AGCGCTGCATCGCCGCCGCCTGCGGCCACGACCGGGACTCCACCTTCGTGGGATGGGCGC  43860
         R  C  I  A  A  A  C  G  H  D  R  D  S  T  F  V  G  W  A  P

43861  CGTTCTTCCACGACATGGGCCTGGTCGCCAACCTCCTCCAGCCCCTCTACCTCGGGTCCC  43920
         F  F  H  D  M  G  L  V  A  N  L  L  Q  P  L  Y  L  G  S  L

43921  TGTCGGTGCTGATGCCGCCGATGGCCTTCCTCCAGCGCCCGGCCCGCTGGCTGCGGGCCG  43980
         S  V  L  M  P  P  M  A  F  L  Q  R  P  A  R  W  L  R  A  V

43981  TCTCCCGCTACCGGGCGCACACCAGCGGCGGCCCCAACTTCGCCTACGACCTGTGTGTCG  44040
         S  R  Y  R  A  H  T  S  G  G  P  N  F  A  Y  D  L  C  V  D

44041  ACCGGGTCGGCGAGGACGAGCGGGCCGGACTGGACCTGTCGGGCTGGAAGGTCGCCTACA  44100
         R  V  G  E  D  E  R  A  G  L  D  L  S  G  W  K  V  A  Y  N

44101  ACGGCGCGGAACCTGTACGGGCCGACACCCTGCGACGGTTCACCGACCGCTTCGCCCCCC  44160
         G  A  E  P  V  R  A  D  T  L  R  R  F  T  D  R  F  A  P  H

44161  ACGGCTTCACCCCCGGCGCGCACTTCCCGACCTACGGGCTCGCCGAGGCGACCCTGCTCG  44220
         G  F  T  P  G  A  H  F  P  T  Y  G  L  A  E  A  T  L  L  V

44221  TCGCCACCGGCCCCAAGGGAGTGCCGCCCCGCACCCTGACCGCCGACCGCGCCGCCCTGC  44280
         A  T  G  P  K  G  V  P  P  R  T  L  T  A  D  R  A  A  L  R

44281  GCGCCGGCCGGCTCCGGCCCGCCGGGCCCGGCGAGGCCGGCCTGGAACTGGTCGGCAACG  44340
         A  G  R  L  R  P  A  G  P  G  E  A  G  L  E  L  V  G  N  G

44341  GCACCGCCGGCCTCGACACCACCCTCCGGATCGTCGACCCCGCGACCGCGCGGGAGTGCC  44400
         T  A  G  L  D  T  T  L  R  I  V  D  P  A  T  A  R  E  C  P

44401  CGCCCGGAGAGGTCGGCGAGGTCTGGGTGCGCGGCCCGGGCGTGGCACGCGGCTACTTCG  44460
         P  G  E  V  G  E  V  W  V  R  G  P  G  V  A  R  G  Y  F  G

44461  GCCGCCCGCGCGAGTCCGCGCCGCTGCTCGCCGCCCGCCTGCCCGGCGGCGAAGGACCGT  44520
         R  P  R  E  S  A  P  L  L  A  A  R  L  P  G  G  E  G  P  Y

44521  ACCTGCGGACCGGGGACCTGGGCGCCCTGCACGACGGGGAACTCTTCCTCACCGGACGCC  44580
         L  R  T  G  D  L  G  A  L  H  D  G  E  L  F  L  T  G  R  H

44581  ACAAGGACCTCATCGTCATCCGCGGCCAGAACCACCACCCGCACGACCTCGAACGGACCG  44640
         K  D  L  I  V  I  R  G  Q  N  H  H  P  H  D  L  E  R  T  A

44641  CCGAGCAGGCCCACCCGGCGCTCCGCCCGACCTGCGCCGCCGCGTTCGCGGTGCCCGGGG  44700
         E  Q  A  H  P  A  L  R  P  T  C  A  A  A  F  A  V  P  G  D

44701  ACGGCGCGGAGCGGCTCGTGCTCGTCTGCGAACTCACCTCCTACCGCGCCGTCGACCCGG  44760
         G  A  E  R  L  V  L  V  C  E  L  T  S  Y  R  A  V  D  P  A

44761  CCGCCGTCGCCGAGGCCGTCCGGGCCGCGCTCGCCGCGCGGCACGGCGTCGCCCCGCACA  44820
         A  V  A  E  A  V  R  A  A  L  A  A  R  H  G  V  A  P  H  T

44821  CGCTGGTGGTGCTGCGCCGCGGCGGCATCCCCAAGACCACCAGCGGAAAGGTGCGGCGCG  44880
         L  V  V  L  R  R  G  G  I  P  K  T  T  S  G  K  V  R  R  G

44881  GCCACTGCCGGACGGCCTACCTCGACGGAACGCTCCCCGTTCACACGGCCGTCCGCCTCC  44940
         H  C  R  T  A  Y  L  D  G  T  L  P  V  H  T  A  V  R  L  P

44941  CGGCGGGGGAGGAGGGCACCGAGGCCCTTCCCCTGACCACGGACCCCGGTCGGCTGGCCA  45000
         A  G  E  E  G  T  E  A  L  P  L  T  T  D  P  G  R  L  A  T

45001  CGGCGCTGCGCGACCTGGCCGCCGCCCACGCGGGCCTGGCCGGGCCCCTCCCCGGCACCG  45060
         A  L  R  D  L  A  A  A  H  A  G  L  A  G  P  L  P  G  T  D

45061  ACGAGCCGGTGAGCGCCCTCGGCCTGGACTCGCTCGCCTCCCTGCGGCTCCACCACCACG  45120
         E  P  V  S  A  L  G  L  D  S  L  A  S  L  R  L  H  H  H  V

45121  TCCAGTCCGCCTACGGCGTGACCCTGCCCGTCACCGCCCTGCTCGGCGACACCACTTACC  45180
         Q  S  A  Y  G  V  T  L  P  V  T  A  L  L  G  D  T  T  Y  R

45181  GCCGGCTCGCGGAGCTGACGCTCGCCGCCCCCCGCCCGGCCCGGGCGCCCGAGGGGCAAG  45240
         R  L  A  E  L  T  L  A  A  P  R  P  A  R  A  P  E  G  Q  V
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45241  TCACCGGCGTCTGGCGGCCGTTGACGCACGGGCAGCGCGCCCTGTGGTACGAACAGGCGC  45300
         T  G  V  W  R  P  L  T  H  G  Q  R  A  L  W  Y  E  Q  A  L

45301  TCGCCCCGCACGCGGCCGCCTACCACCTCGTCCGCGCGCTGGCCCTCCGCGGCCCCGTCG  45360
         A  P  H  A  A  A  Y  H  L  V  R  A  L  A  L  R  G  P  V  D

45361  ACGAGGAGGCCCTCGCCGAGGCGGTCCGCCGCGTCGTCCGCCGCCACCCCGCCCTGCGGA  45420
         E  E  A  L  A  E  A  V  R  R  V  V  R  R  H  P  A  L  R  T

45421  CCCGCTTCGCGCTCCGCGACGGCGAACCGGCGCGCCGGACCGAGCCGTACGGACCGGAGC  45480
         R  F  A  L  R  D  G  E  P  A  R  R  T  E  P  Y  G  P  E  L

45481  TGGACGTACGCGACGCCACCGGCCTGCCGGCGGACCGGCTCCGCGAACACCTGGCCGCGG  45540
         D  V  R  D  A  T  G  L  P  A  D  R  L  R  E  H  L  A  A  A

45541  CGGGCGACCGCCCCTTCGACCTGGCCGCCGGCGACAGGCCCGTGAGGCTGACGCTCTACC  45600
         G  D  R  P  F  D  L  A  A  G  D  R  P  V  R  L  T  L  Y  R

45601  GCACGGACGGCGGCCACATCCTGCTGCTGGTCGCCCACCACCTGGTCGCCGACTTCTGGT  45660
         T  D  G  G  H  I  L  L  L  V  A  H  H  L  V  A  D  F  W  S

45661  CCCTCGTCGTCCTCCTGGGCGACCTCGCCCGGGCCCACGCGGGCGAGGACCTGCCGCCCG  45720
         L  V  V  L  L  G  D  L  A  R  A  H  A  G  E  D  L  P  P  A

45721  CGCCGGAGGGGGACCCCGGCGACGAGGCGACGGACGCGGACCGGACGTACTGGCGGCACC  45780
         P  E  G  D  P  G  D  E  A  T  D  A  D  R  T  Y  W  R  H  R

45781  GGCTCGCCGACGCGCCACCCGCCCTCGACCTGCCCACCGACCTCCCCCACCCCGCCGAGC  45840
         L  A  D  A  P  P  A  L  D  L  P  T  D  L  P  H  P  A  E  R

45841  GCGGCTTCGCCGGCGCCACCCACGCCTTCCGGCTGCCCCCGGACCTCACCGCCCGGCTGA  45900
         G  F  A  G  A  T  H  A  F  R  L  P  P  D  L  T  A  R  L  T

45901  CCGCCCTCTCCCGGGAACGGCACTGCACCCTCTTCACCACCCTCCTCGCCGCCCACCAGC  45960
         A  L  S  R  E  R  H  C  T  L  F  T  T  L  L  A  A  H  Q  L

45961  TACTGCTCCACCGCCTGACCGGGCAGGACGACCTCGTCGTGGGCACCCTCCTCGCCCGCC  46020
         L  L  H  R  L  T  G  Q  D  D  L  V  V  G  T  L  L  A  R  R

46021  GCGACACCGCCGAAGCGGCCGGCGCCGTCGGCTACCTGGTCAACCCGCTGCCGCTGCGCT  46080
         D  T  A  E  A  A  G  A  V  G  Y  L  V  N  P  L  P  L  R  S

46081  CCGTACGGGAGCCGGGGGAGACCTTCACGGAACTGCTGCGCCGCACCCGGCGGACCGTGC  46140
         V  R  E  P  G  E  T  F  T  E  L  L  R  R  T  R  R  T  V  L

46141  TGGACGCGGTCGCGCACGGCCGCCACCCCTTCGGGCCGCTCGTCTCCCGTCTCGCCCCCG  46200
         D  A  V  A  H  G  R  H  P  F  G  P  L  V  S  R  L  A  P  A

46201  CGCGCACGCCCGGCCGCGCGCCGCTCCTGCAGAGCCTGTTCGTGCTCCAGCGCGAGTACG  46260
         R  T  P  G  R  A  P  L  L  Q  S  L  F  V  L  Q  R  E  Y  G

46261  GCGACGAGGCGGACGGGTACCGCGCGCTCGCCCTGGGCGTCGGCGGCCGGCTGCGCGTCG  46320
         D  E  A  D  G  Y  R  A  L  A  L  G  V  G  G  R  L  R  V  G

46321  GCGGACTCGACCTGGAGGCACTCGCGTTGCCGCGCCGCTGGTCGCAGCTCGACCTCTCGC  46380
         G  L  D  L  E  A  L  A  L  P  R  R  W  S  Q  L  D  L  S  L

46381  TGAGCATGGCGCGGCTCGGGGACGGGCTGACGGGGGTGTGGGAGTACCGCACCGACCTGT  46440
         S  M  A  R  L  G  D  G  L  T  G  V  W  E  Y  R  T  D  L  F

46441  TCACCGAGGCCACGGTCGCGGAGCTGAGCGAGGCGTTCGTCCACCTGCTGCGGGCGGCCG  46500
         T  E  A  T  V  A  E  L  S  E  A  F  V  H  L  L  R  A  A  V

46501  TCGAGGACCCGGGCGCGCCCGTGGAGACGCTGCCGCTCACCGGCGGCCGGGAGACCGGGC  46560
         E  D  P  G  A  P  V  E  T  L  P  L  T  G  G  R  E  T  G  P

46561  CGCGCCGCGGCCCGTCGGCGGCCCGGCCCGCCCTCCCGCTGCACCGGCTCGTGGCCGCGG  46620
         R  R  G  P  S  A  A  R  P  A  L  P  L  H  R  L  V  A  A  A

46621  CGGCGCGCCGCGATCCCGCACGGACGGCGGTCGTCGCACTCGCCCCGGACGGCACCGCCC  46680
         A  R  R  D  P  A  R  T  A  V  V  A  L  A  P  D  G  T  A  H

46681  ACCACATCAGCCACGGAGCCCTGCACCGCGCGGCCACCACCCTCGCCGCCCGGCTCCGCC  46740
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H I S H G A L H R A A T T L A A R L R R

46741 GGGAGGGCGCCGGCCCGGAGCGGCCCGTCGCCGTGCTCGTCGAGCGGGGCCCCTGGCTGC 46800
E G A G P E R P V A V L V E R G P W L P

46801 CCGTCGCCTACCTCGGCATCCTGCACGCCGGGGCCACCGTGCTGCCCCTGGACCCGGAGG 46860
V A Y L G I L H A G A T V L P L D P E D

46861 ACCCCCCGCACAGGCTCGCCCGGACGATCGCGAACTCGGGGGCGCGGCTGCTGCTCACCG 46920
P P H R L A R T I A N S G A R L L L T E

46921 AGACCGGGACCGCCTCGCGCGCGGCCGAGGCGGCCGGTCCCGGCGTACGCGCGCTGACCG 46980
T G T A S R A A E A A G P G V R A L T V

46981 TGCGTGAGGGTGCCACCGGCGGCGAGCGGTTCTCGGCGGACGTCCACCCCGAGCAGTCCG 47040
R E G A T G G E R F S A D V H P E Q S A

47041 CGTACCTGCTGTACACCTCCGGGTCGACGGGCGACCCCAAGGGCGTGCTCGTCCCGCACC 47100
Y L L Y T S G S T G D P K G V L V P H R

47101 GGGCCATCGTCAACCGCCTCCTGTGGATGCAGGAGACCTACCGGCTGCGCCCGGGGGAGC 47160
A I V N R L L W M Q E T Y R L R P G E R

47161 GGGTCCTGCACAAGACGCCGGTGACGTTCGACGTCTCGATGTGGGAGCTGCTGTGGCCGC 47220
V L H K T P V T F D V S M W E L L W P L

47221 TGACCGCCGGGGCGACCGTCGTCATGGCCCGGCCCGGGACCCACCGCGACCCCGCGCGAC 47280
T A G A T V V M A R P G T H R D P A R L

47281 TCGTCCGGCGGATCGCCCGCGAGGCCGTCACCACCGTGCACTTCGTCCCCTCGATGCTCA 47340
V R R I A R E A V T T V H F V P S M L T

47341 CCCCGTTCCTCACCGAGCTCGCCCGCGGCACGACGCGGCTGCCCGCGCTGCGGCGCGTGG 47400
P F L T E L A R G T T R L P A L R R V V

47401 TGTGCAGCGGGGAAGAGCTGCCCGCGGCCGCGGTGAACCGCGCCGCCGGACTCCTCGACG 47460
C S G E E L P A A A V N R A A G L L D A

47461 CCCGGCTGTACAACCTCTACGGCCCGACCGAAGCCGCCGTCGACGTCACCGCCTGGCCCT 47520
R L Y N L Y G P T E A A V D V T A W P C

47521 GCCGCCCGCCCGAGCCGGGGCCGGTGCCGATCGGCCTGCCCATCGCCAACACCACCACCG 47580
R P P E P G P V P I G L P I A N T T T E

47581 AGGTCCTCGACGGCCGGCTGCGCCCGCTGCCCCGCCCGGTGCCCGGCGAGCTGTACCTGG 47640
V L D G R L R P L P R P V P G E L Y L G

47641 GCGGCGCCTGCCTGGCCCATGGCTACCACCACGACCCGGCCCTGACCGCCGCGCGCTTCC 47700
G A C L A H G Y H H D P A L T A A R F L

47701 TTCCGGCCCCCGGCGGCGGGCGCCGCTACCGCACCGGGGACCTCGTCCGCCAACGGGCCG 47760
P A P G G G R R Y R T G D L V R Q R A D

47761 ACGGGGCACTGGTGTTCCGGGGACGCACGGACGACCAGGTGAAGATCGGCGGCATCCGGG 47820
G A L V F R G R T D D Q V K I G G I R V

47821 TCGAGCCCGGCGAGGTGGCGGAGGCGCTTCGGGCCCTGCCCGGCGTCGCCGACGCCGCGG 47880
E P G E V A E A L R A L P G V A D A A V

47881 TCGTCCCGCACGACGGGCGGCTGGCGGCGTACGCGGTCGCCGACCCGGTCGGCCCGGCCC 47940
V P H D G R L A A Y A V A D P V G P A P

47941 CGGCGGCGGACGCCCTGCGGGACGCGCTGCGCAGGCGGCTGCCCGGCCACCTGGTGCCCG 48000
A A D A L R D A L R R R L P G H L V P A

48001 CCGCCCTCACCCTGCTGGACCGGCTGCCCCTCACCCCGGCGGGCAAGCTCGACCGCCGGG 48060
A L T L L D R L P L T P A G K L D R R A

48061 CGCTGCCCCACCCGTCGGCCCCGCCCCCGGACGGCGGACGGCCGCCCACGACCGGGACCG 48120
L P H P S A P P P D G G R P P T T G T E

48121 AACGGCTCGTCGCCCGGGTGTGGGCCGAACGCCTCGGACGGGAAGTCGTCGGCGTGGACC 48180
R L V A R V W A E R L G R E V V G V D R

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48181  GGGACTTCTTCTCCCTGGGCGGCGACTCCGTCCGGGCCCTCGGCGTGACGGCGGCCCTGC  48240
         D  F  F  S  L  G  G  D  S  V  R  A  L  G  V  T  A  A  L  R

48241  GCGCCGCCGGGCTCCCGGTGACGGTCACCGACCTCCTGCGCCTGCCCACCGTGGCCGCCC  48300
         A  A  G  L  P  V  T  V  T  D  L  L  R  L  P  T  V  A  A  L

48301  TCGCCCGCCACGCCGACGAGCGGGCGGATCGCCGACCGGCGCGACAGGAGACGCCCCCCG  48360
         A  R  H  A  D  E  R  A  D  R  R  P  A  R  Q  E  T  P  P  G

48361  GGCCGTTCGCCCTCTGCCCGGAAGCCGCCGGCGTGCCCGGCCTGGAGGACGCCTACCCGA  48420
         P  F  A  L  C  P  E  A  A  G  V  P  G  L  E  D  A  Y  P  M

48421  TGTCGATGGCCCAGCGGGCCGTGCTCTTCCACCGTGACCACAACCCCGGCTACGAGGTCT  48480
         S  M  A  Q  R  A  V  L  F  H  R  D  H  N  P  G  Y  E  V  Y

48481  ACGTCACCAGCGTCGCCGTCTCCACGCCCCTGGACCGCACACGGCTCGCCGCGGCCGTGG  48540
         V  T  S  V  A  V  S  T  P  L  D  R  T  R  L  A  A  A  V  D

48541  ACCGGCTGCTGGACCGGCACGCCTATCTGCGGTCCTCCTTCGACCTCGTGTCCCACCCGG  48600
         R  L  L  D  R  H  A  Y  L  R  S  S  F  D  L  V  S  H  P  E

48601  AGCCCACCCAGCTCGTCTGGACCCACCTGCCCACCCCGCTCGAGGTGGTGGAGTCGTCCG  48660
         P  T  Q  L  V  W  T  H  L  P  T  P  L  E  V  V  E  S  S  D

48661  ACCCCGCCGGTTTCGACGCGTGGCTGCACGCCGAACGCAAGCGCCCCCTCGACGTCGGCA  48720
         P  A  G  F  D  A  W  L  H  A  E  R  K  R  P  L  D  V  G  T

48721  CCGGACCGCTGGCCCGGTTCACCGCGCACGACGCGGGAGCCGCCGGATTCCGGCTGACCG  48780
         G  P  L  A  R  F  T  A  H  D  A  G  A  A  G  F  R  L  T  V

48781  TCAGCAGCTTCGCCCTCGACGGCTGGTGCGTGGCCACCGTGCTCACCGAACTGCTCCGCG  48840
         S  S  F  A  L  D  G  W  C  V  A  T  V  L  T  E  L  L  R  D

48841  ACTACTGGTCCGCGCTGCGCGGCGCGCCCCTCAGCCTCCCGGCACCCGCCGCCTCCTACC  48900
         Y  W  S  A  L  R  G  A  P  L  S  L  P  A  P  A  A  S  Y  R

48901  GCGAGTTCGTCGCCCTCGAACGCGCCGCCCAACACGATCCGGCGCACCGGGAGTTCTGGC  48960
         E  F  V  A  L  E  R  A  A  Q  H  D  P  A  H  R  E  F  W  R

48961  GGACGGAGCTCGCCGGTGCCCGGCCGCATCCGCTGCCCCGCCGCCCGGTGCCACCGCCCG  49020
         T  E  L  A  G  A  R  P  H  P  L  P  R  R  P  V  P  P  P  G

49021  GGCCGGACGGGATCCGCCAGCACCGTCACGTCGTCCCCGTCGAGGACACCGTCGCCAAGG  49080
         P  D  G  I  R  Q  H  R  H  V  V  P  V  E  D  T  V  A  K  G

49081  GCCTGTCGGCGCTCGCCGGCGAGCTGGGTGTCGGGCTCAAACACGTTCTGCTCGGCGTCC  49140
         L  S  A  L  A  G  E  L  G  V  G  L  K  H  V  L  L  G  V  H

49141  ACCTGCGGGTCGTCCGGGCCCTGTCCGGCGACCCCGACGTCATCACGGCCGTGGAGACCC  49200
         L  R  V  V  R  A  L  S  G  D  P  D  V  I  T  A  V  E  T  H

49201  ACGGCCGCCTCGAACGGCACGACGGCGACCGCGTCCTCGGGGTGTTCAACAACATCCTGC  49260
         G  R  L  E  R  H  D  G  D  R  V  L  G  V  F  N  N  I  L  P

49261  CGCTGCGGCAGCGGGTGGACGGCGGGAGCTGGGCCGACCTGGCCCGCGCCGCGCACGCCG  49320
         L  R  Q  R  V  D  G  G  S  W  A  D  L  A  R  A  A  H  A  A

49321  CGGAGGCGCGGACGGGGGAGTACCGCCGCTATCCGCTGGCCCAGGCACAGCGCGACCACG  49380
         E  A  R  T  G  E  Y  R  R  Y  P  L  A  Q  A  Q  R  D  H  G

49381  GCGCGGCCGGGCTCTTCGACACCCTCTTCGTGTTCACCCACTTCCACCTCTACCGCGCGC  49440
         A  A  G  L  F  D  T  L  F  V  F  T  H  F  H  L  Y  R  A  L

49441  TGGCCGACCTGGACGGCATGGCGGTCTCCGACCTGCGGGCCCCCGACCAGACCTACGTAC  49500
         A  D  L  D  G  M  A  V  S  D  L  R  A  P  D  Q  T  Y  V  P

49501  CGCTCACCGCCCACTTCAACGTCGACGCCACGGACGGCGGCGGCCTGCGGCTGCTGCTGG  49560
         L  T  A  H  F  N  V  D  A  T  D  G  G  G  L  R  L  L  L  E

49561  AGTCGGACCCGCGGGAGTTCCCCGACGAGCAGGTCGCGGAGTTCGCCGCGTACTACCGCC  49620
         S  D  P  R  E  F  P  D  E  Q  V  A  E  F  A  A  Y  Y  R  R

49621  GCGCGCTGCGGGCCGCCGCCGACGCCCCGCACCGGCCGTACCGGGACACGCCGTTGACGG  49680
         A  L  R  A  A  A  D  A  P  H  R  P  Y  R  D  T  P  L  T  D
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49681  ACCGGCCGGCCGGTCCGGCGCCGCACCGCGCGGAGCGCTCCGTCCACGCCCTGTTCGCGG  49740
         R  P  A  G  P  A  P  H  R  A  E  R  S  V  H  A  L  F  A  A

49741  CCCCGGCCCGGAACCACCCGGACCGGATCGCGCTCGACGGCGAGGACGGGCCGGTCAGCC  49800
         P  A  R  N  H  P  D  R  I  A  L  D  G  E  D  G  P  V  S  H

49801  ACGGCGCCCTGGCCCGGCGCGCCGCCCGCCTCGCCGGAACGCTGCGGGCCGCGGGCGCCG  49860
         G  A  L  A  R  R  A  A  R  L  A  G  T  L  R  A  A  G  A  G

49861  GGCCGGACACCGTCGTCGGGATCTGGGCGCCGCGCCGCGCCGACGCCGTCGTGGCGCTGC  49920
         P  D  T  V  V  G  I  W  A  P  R  R  A  D  A  V  V  A  L  L

49921  TGGCCGCCCTCCACGCCGGAGCCGCCTACCTGCCCCTGGACCCGGTCCACCCGCCCCGGC  49980
         A  A  L  H  A  G  A  A  Y  L  P  L  D  P  V  H  P  P  R  R

49981  GGCAGCGGCAGGTGCTCACCGAGGCCGGCGCCCGCCTGCTCGTCCTGCCCGCCGGCCTCG  50040
         Q  R  Q  V  L  T  E  A  G  A  R  L  L  V  L  P  A  G  L  D

50041  ACACCCCGCTCCGGGCCTGCGGCCTGCCCGTCGTGGCCCCGGACGACCTCGGCGCGCCCA  50100
         T  P  L  R  A  C  G  L  P  V  V  A  P  D  D  L  G  A  P  I

50101  TCGCCCCCGTGTCCGTCCACCCGGAGCAGCTGGCGGCGGTCATGGCCACGTCCGGCTCCA  50160
         A  P  V  S  V  H  P  E  Q  L  A  A  V  M  A  T  S  G  S  T

50161  CCGGGACGCCCAAGACGATCGGCGTCCCGCAGCGCGCCCTGGCCGGCTACCTCCGCTGGG  50220
         G  T  P  K  T  I  G  V  P  Q  R  A  L  A  G  Y  L  R  W  A

50221  CGATCGGCCACTACCGCCTCGACGAGGAGACCGTCTCCCCGGTGCACTCCTCGCTGGGCT  50280
         I  G  H  Y  R  L  D  E  E  T  V  S  P  V  H  S  S  L  G  F

50281  TCGACCTGACCGTCACCGCGCTGCTCGCACCGCTGGCCGCCGGCGGGCAGGCGCGGCTGA  50340
         D  L  T  V  T  A  L  L  A  P  L  A  A  G  G  Q  A  R  L  T

50341  CCGACTCCGGCGACCCGGGTGCCCTCGGCGCGGCACTGGCCGCCGGCCACCACACCCTGC  50400
         D  S  G  D  P  G  A  L  G  A  A  L  A  A  G  H  H  T  L  L

50401  TCAAGATCACCCCGGCCCATCTGGCCGCCCTCGCCCACCAGTTGGGCGCGCCGACCGCAC  50460
         K  I  T  P  A  H  L  A  A  L  A  H  Q  L  G  A  P  T  A  L

50461  TGCGCACCGTCGTGGCCGGGGGCGAACCCCTGCACGCCGGCCACGTCCGCGCCCTCCGCG  50520
         R  T  V  V  A  G  G  E  P  L  H  A  G  H  V  R  A  L  R  A

50521  CCTTCGCGCCCGGCGCCCGGCTCGTCAACGAGTACGGGCCGACCGAGACCACCGTCGGCT  50580
         F  A  P  G  A  R  L  V  N  E  Y  G  P  T  E  T  T  V  G  C

50581  GCTGTGCCCACGACGTCGCACCGGACCCCGGCGAGGCGCCCATCCCCGTCGGTACCCCGA  50640
         C  A  H  D  V  A  P  D  P  G  E  A  P  I  P  V  G  T  P  I

50641  TCGCGGGCCTCAGCGCGTGCGTCGTCGACGACGCGCTGCCCGCACCGCCCGGCGTGCGGG  50700
         A  G  L  S  A  C  V  V  D  D  A  L  P  A  P  P  G  V  R  G

50701  GCGAGCTGTACATCGGCGGGACGGGCGTCACCCGCGGCTACCTGGGCCGGCCCGCGGCCA  50760
         E  L  Y  I  G  G  T  G  V  T  R  G  Y  L  G  R  P  A  A  T

50761  CCGCCGCCGCCTACGTGCCGGACCCTGCCGCCCCCGGCGCCCGCCGCTACCGCACCGGCG  50820
         A  A  A  Y  V  P  D  P  A  A  P  G  A  R  R  Y  R  T  G  D

50821  ACCTGGCACGCCGGCTGCCGGACGGCACCCTGCTCCTGGCGGGGCGCGCCGACCGCCAGG  50880
         L  A  R  R  L  P  D  G  T  L  L  L  A  G  R  A  D  R  Q  V

50881  TGAAGATCCGCGGCCACCGGGTGGAACCGGGGGAGGTCGAGCAGGTGCTCGGCGGCCACC  50940
         K  I  R  G  H  R  V  E  P  G  E  V  E  Q  V  L  G  G  H  P

50941  CCGGGGTGCGGGAGGCGGCGGTCGTCGCCCACCCGGCACCCGGCGGCGGCCGCCGGCTGG  51000
         G  V  R  E  A  A  V  V  A  H  P  A  P  G  G  G  R  R  L  V

51001  TCGCGTACTGGGTACCGGCCGAACCGGCCCGGCCACCGTCCGCGGACGCGCTCACCGCGC  51060
         A  Y  W  V  P  A  E  P  A  R  P  P  S  A  D  A  L  T  A  L

51061  TGCTCGCCGACCGGCTGCCGCCGTACGCGGTCCCCGCCGAACTCGTCCGCCTGCCCGCCC  51120
         L  A  D  R  L  P  P  Y  A  V  P  A  E  L  V  R  L  P  A  L

51121  TGCCCACCACCCCCAACGGCAAGGTCGACCACACCCGGCTGCCCGCGGCCGGACGGGACC  51180
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          P  T  T  P  N  G  K  V  D  H  T  R  L  P  A  A  G  R  D  R
51181 GGCGACTGGCGGAACTGCTCGACCGGATCGAGGCACTGTCCGACGCCGAGGCGGCCTCGG 51240
          R  L  A  E  L  L  D  R  I  E  A  L  S  D  A  E  A  A  S  A
51241 CACTGCGCGACAGCCGGCCCGCACCCGGGAGTGGCGATGACCGAGCATGACGACCACCCG 51300
          L  R  D  S  R  P  A  P  G  S  G  D  D  R  A  *
51301 CCGGCCCGCCGGGGCCCCGCCGGTTCCGCTGGCCCCGGCGGAAGCCCGCCCGTCCCGCAC 51360
51361 GTGCCGGTGCCCGGGCATGACGACCGCGTCGGACGGCTGCCGGCGGACCGGAGCGTCCCG 51420
51421 CCGACCCGCCGATTCTCTGGGGACCCCGCCGGTTCCGGTGGTGGCCCGCCCGTCCCGCAC 51480
51481 CCGGAGGTGCCGATGCGCGGGCATGACGACCGCGTCGGACGGCTGTCGGCGGACTGGAGC 51540
                M  R  G  H  D  D  R  V  G  R  L  S  A  D  W  S    (orf21)
51541 GTCCCGCCGACCCGCCTGCCCGCCGGGGACCCGGCCGGTTCCGTCGGCCCCGGCGGAGGC 51600
          V  P  P  T  R  L  P  A  G  D  P  A  G  S  V  G  P  G  G  G
51601 CCGCCCGTCCCGCACGAGGAGGTGACGATGTCGGAGTATGACGACCGCCTCGCGCGGCTG 51660
          P  P  V  P  H  E  E  V  T  M  S  E  Y  D  D  R  L  A  R  L
51661 TCGGACAACCAGCGCGCCCTGCTGGACCGCTGGCTCGCCGAGGACCCCGCCGGCGGTGCC 51720
          S  D  N  Q  R  A  L  L  D  R  W  L  A  E  D  P  A  G  G  A
51721 GGCCCGCTTCGCCCCGACGGCCGCCCGCCCCGCACCGAGGCCGAGCGGATCCTGGCCGGG 51780
          G  P  L  R  P  D  G  R  P  P  R  T  E  A  E  R  I  L  A  G
51781 GTCTGGGAGGAGGTGCTGGAGACCGGCGGGATCGGCGCCGACGACGACTACTTCGCGCTC 51840
          V  W  E  E  V  L  E  T  G  G  I  G  A  D  D  D  Y  F  A  L
51841 GGCGGAGACTCCGTCCACGCCATCGTCATCGTGGCGAAGGCCCGGCAGGCCGGACTCGCC 51900
          G  G  D  S  V  H  A  I  V  I  V  A  K  A  R  Q  A  G  L  A
51901 CTGACCGCCCATGACCTCTTCGAGGCCAGGACCCTCGCGGCCGTGGCGCGGAGAGCCGCC 51960
          L  T  A  H  D  L  F  E  A  R  T  L  A  A  V  A  R  R  A  A
51961 CCGGCCGGCCCCGCCGAGCCCGTCCCCGACGCGGGCGGCGGCGCGGTCCGGTACCCGCTG 52020
          P  A  G  P  A  E  P  V  P  D  A  G  G  G  A  V  R  Y  P  L
52021 ACCCCTATGCAGCAGGGCATGCTCTACCACTCGGCCGGCGGCAGCACGCCCGGCGCCTAC 52080
          T  P  M  Q  Q  G  M  L  Y  H  S  A  G  G  S  T  P  G  A  Y
52081 GTGGTGCAGGTGTGCTGCCGGCTGACGGGGGACCTCGACGTGGCCGCCTTCCGCACCGCC 52140
          V  V  Q  V  C  C  R  L  T  G  D  L  D  V  A  A  F  R  T  A
52141 TGGCAGGCCGTGCTGTCCGCCAACCCGGCGCTGGCCGTCTCCTTCCACTGGTCCGACGGC 52200
          W  Q  A  V  L  S  A  N  P  A  L  A  V  S  F  H  W  S  D  G
52201 TCCCCGCCCGAGCAGGTGGTGGACCCCGACGCGCGCGTCACCGTCGACACGGCCGACTGG 52260
          S  P  P  E  Q  V  V  D  P  D  A  R  V  T  V  D  T  A  D  W
52261 CGGGACCGCACCCCGGCCGAGCGGGACGATGCCTTCGCCCGCTTCCTGGACACCGACCGC 52320
          R  D  R  T  P  A  E  R  D  D  A  F  A  R  F  L  D  T  D  R
52321 GCGGCGGGCTTCGACCTCGCCCGCGCCCCGCTGATGCGGCTGACGCTCTTCCGCGAGGGC 52380
          A  A  G  F  D  L  A  R  A  P  L  M  R  L  T  L  F  R  E  G
52381 GAGCACGCGTACCGCTGCGTGTGGACCCACCACCACCTCGTCCTCGACGGCTGGTCCCAG 52440
          E  H  A  Y  R  C  V  W  T  H  H  H  L  V  L  D  G  W  S  Q
52441 CAGCTCGTCCTGCGCGACGTCCTCGACTGCTACATGCGCCTGCGCGCCGGACGCGGCGCC 52500
          Q  L  V  L  R  D  V  L  D  C  Y  M  R  L  R  A  G  R  G  A
52501 GAGCCGCCCGCCCGGCCGTCCTTCACCGGTCATCTGCGCCGGCTGGAGCGGCAGGACGGG 52560
          E  P  P  A  R  P  S  F  T  G  H  L  R  R  L  E  R  Q  D  G
52561 ATCGACGAGGAGTTCTGGCGCGACCACCTCGGCGGCCTGCCCGCACCCTCCCGCGTCGCC 52620
          I  D  E  E  F  W  R  D  H  L  G  G  L  P  A  P  S  R  V  A
52621 GGTCCCGGCTGCCGCGACGGCCGGGTGGTCGCCGTACGGCGCGCCGAGCACCGGCACCGG 52680
          G  P  G  C  R  D  G  R  V  V  A  V  R  R  A  E  H  R  H  R
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52681  GTCTCCGCGGCGACGGGCCGGGAGCTGACCGGCTTCTGCCGCCGCCACGGGCTGACCCCG   52740
       V  S  A  A  T  G  R  E  L  T  G  F  C  R  R  H  G  L  T  P
                .     .     .     .     .     .     .     .     .
52741  GCCGCCGTGCTGCACGGCGGCTGGGCGGTGCTGCTGTCGCTGCACTGCGGCCAGGACGAC   52800
       A  A  V  L  H  G  G  W  A  V  L  L  S  L  H  C  G  Q  D  D
                .     .     .     .     .     .     .     .     .
52801  GTGGTCTTCGGCACCACCCTCTCCGGCCGCCCCGAGGACCTGCCCGGCGTGACCGAGTGC   52860
       V  V  F  G  T  T  L  S  G  R  P  E  D  L  P  G  V  T  E  C
                .     .     .     .     .     .     .     .     .
52861  GTCGGCCTCTTCATCAACACGCTTCCCCTGCGGGTCCGTTGCGGGGAGGACACGGACGTC   52920
       V  G  L  F  I  N  T  L  P  L  R  V  R  C  G  E  D  T  D  V
                .     .     .     .     .     .     .     .     .
52921  GTCGACTGGCTCCACGGCGTCCAAAGCGACCTGGCCGCCCTGTGGGACCACGCGCACGTc   52980
       V  D  W  L  H  G  V  Q  S  D  L  A  A  L  W  D  H  A  H  V
                .     .     .     .     .     .     .     .     .
52981  CCGCTCAGCCGCGTcGAGCGCGGTCTCGGACTGGGCCGGgGCGGCGGGCTGTTCGACAGC   53040
       P  L  S  R  V  E  R  G  L  G  L  G  R  G  G  G  L  F  D  S
                .     .     .     .     .     .     .     .     .
53041  ATCATGGTCGTCGAGAACTTCCCCGCCGCCGTCGCCGACGGCCACGAGGCGGgCGGGCTG   53100
       I  M  V  V  E  N  F  P  A  A  V  A  D  G  H  E  A  G  G  L
                .     .     .     .     .     .     .     .     .
53101  CGGGTGACGGAGCCCCGGGCACTCGTCGACGAGGGCTACCCCCTCGTACTGGAGGCCACC   53160
       R  V  T  E  P  R  A  L  V  D  E  G  Y  P  L  V  L  E  A  T
                .     .     .     .     .     .     .     .     .
53161  ACCGGGGACCGGCCGGTGCTGCACGCCCGCTACGACCCCCACCGCCTCGCCGGCGGGCGG   53220
       T  G  D  R  P  V  L  H  A  R  Y  D  P  H  R  L  A  G  G  R
                .     .     .     .     .     .     .     .     .
53221  GTCCAGGCGCTGCTCGCCGCCTTCGACGACTACCTCCGGGCGGTGACCGCCGACCCGGCC   53280
       V  Q  A  L  L  A  A  F  D  D  Y  L  R  A  V  T  A  D  P  A
                .     .     .     .     .     .     .     .     .
53281  CGCCCGCTGCCGGACCTCCGCGCGGTCCTGGCCCGCGACCACGCGCGCCGGGACGGCGCG   53340
       R  P  L  P  D  L  R  A  V  L  A  R  D  H  A  R  R  D  G  A
                .     .     .     .     .     .     .     .     .
53341  GCACGCGGGCGGCGCCGCGCCGCGGACCGCACCCGTCTGACGCTGGCCCGCCGCCGCCCG   53400
       A  R  G  R  R  R  A  A  D  R  T  R  L  T  L  A  R  R  R  P
                .     .     .     .     .     .     .     .     .
53401  GCGACGACGACCGAGGGAGAGACACCGTGACATGGACCGTGGTGACCGGAGCCGGCGGCT   53460
       A  T  T  T  E  G  E  T  P  *
                                  M  T  W  T  V  V  T  G  A  G  G  F   (orf20)
                .     .     .     .     .     .     .     .     .
53461  TCATCGGCTCCCACCTCGTACGCCGCCTCGTCCGGGACGGGCACCGGGTCCGCGGCGTGG   53520
         I  G  S  H  L  V  R  R  L  V  R  D  G  H  R  V  R  G  V  D
                .     .     .     .     .     .     .     .     .
53521  ACCTGGTGCCGCCGCGCTACGGCCCCGGCGAGGCCCAGGAGTTCGTCATCGCCGACCTGC   53580
         L  V  P  P  R  Y  G  P  G  E  A  Q  E  F  V  I  A  D  L  R
                .     .     .     .     .     .     .     .     .
53581  GCGACGCGGCGCAGGCCGCGCGGGCCGTCGCCGGCGCGGACTCCGTCTTCGCGCTCGCGG   53640
         D  A  A  Q  A  A  R  A  V  A  G  A  D  S  V  F  A  L  A  A
                .     .     .     .     .     .     .     .     .
53641  CCAACATGGGAGGCATCGGCTGGACCCACACCGCGCCCGCCGAGATCCTCCACGACAACC   53700
         N  M  G  G  I  G  W  T  H  T  A  P  A  E  I  L  H  D  N  L
                .     .     .     .     .     .     .     .     .
53701  TGCTGATCTCCACCCACACCATCGAGGCATGCCGGGCCGCCGGCGTGCGCACCACCGTCT   53760
         L  I  S  T  H  T  I  E  A  C  R  A  A  G  V  R  T  T  V  Y
                .     .     .     .     .     .     .     .     .
53761  ACACCTCCTCGGCCTGCGTCTACCCCGCGTCCCTGCAGCGCGAGCCCGACGCCGCGCCGC   53820
         T  S  S  A  C  V  Y  P  A  S  L  Q  R  E  P  D  A  A  P  L
                .     .     .     .     .     .     .     .     .
53821  TGGCCGAGGACCCGGTCTTCCCCGCGGAACCCGACATGGAGTACGGCTGGGAGAAGCTGA   53880
         A  E  D  P  V  F  P  A  E  P  D  M  E  Y  G  W  E  K  L  T
                .     .     .     .     .     .     .     .     .
53881  CCACGGAAATCCTGTGCGGCGCCTACCGCCGCAGCCACGGCATGGACATCAAGACAGCCC   53940
         T  E  I  L  C  G  A  Y  R  R  S  H  G  M  D  I  K  T  A  R
                .     .     .     .     .     .     .     .     .
53941  GGCTGCACGCCATCTACGGCCCCCTCGGCACGTACACCGGGCCCCGCGCGAAGTCCCTGT   54000
         L  H  A  I  Y  G  P  L  G  T  Y  T  G  P  R  A  K  S  L  S
                .     .     .     .     .     .     .     .     .
54001  CGATGCTCTGCGACAAGGTCGCCCGGATACCCGGCGACGAGGGGGAGATAGAGGTCTGGG   54060
         M  L  C  D  K  V  A  R  I  P  G  D  E  G  E  I  E  V  W  G
                .     .     .     .     .     .     .     .     .
54061  GGGACGGGACGCAGACCCGCTCCTACTGTTACGTCGACGACTGTGTCGAAGGGCTGATCC   54120
         D  G  T  Q  T  R  S  Y  C  Y  V  D  D  C  V  E  G  L  I  R
                .     .     .     .     .     .     .     .     .
54121  GGCTCGCCCGCTCCGACGTGGCGGAACCGGTCAACATCGGCTCCGAGGAGCGCGTCGACA   54180
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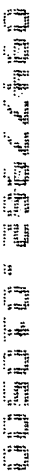

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          L  A  R  S  D  V  A  E  P  V  N  I  G  S  E  E  R  V  D  I
54181 TCGCGTCGCTCGTCGAGCGGATCGCCGGGGTCGCCGGGAAGAAGGTGCGCTGCGCCTTCG 54240
          A  S  L  V  E  R  I  A  G  V  A  G  K  K  V  R  C  A  F  A
54241 CCCCCGACCGCCCGGTCGGGCCCCGCGGGCGCGTCTCGGACAACACCCGCTGCCGCGAAC 54300
          P  D  R  P  V  G  P  R  G  R  V  S  D  N  T  R  C  R  E  L
54301 TGCTCGGCTGGGCACCGGAGACGTCCCTCGCGGCCGGCCTGGAGCGCACCTACCCGTGGA 54360
          L  G  W  A  P  E  T  S  L  A  A  G  L  E  R  T  Y  P  W  I
54361 TCGAGCGCCAGGTCCTCGCCGAGGCCGGGAGGGCCGATGCCTGAGCACCGCACACCGGTG 54420
                                                                  M    (orf19)
          E  R  Q  V  L  A  E  A  G  R  A  D  A  *
54421 AAGGACCTCGGCCGGCTGCTGCTCGGGCACGCCGCGCGCTTCCGGGGCCGCGAGCTGCAG 54480
          K  D  L  G  R  L  L  L  G  H  A  A  R  F  R  G  R  E  L  Q
54481 GACGTCGCCACCCGGGCGCTGCGGGCCTCCGGCGGGGAGAACGCCTGGGTGGTGTCCGTC 54540
          D  V  A  T  R  A  L  R  A  S  G  G  E  N  A  W  V  V  S  V
54541 GTCAACACCAGTCTCCGCGCCCGCCAGGCCGTGGACCACGCGCTGCGGCTCGCCCCCCGC 54600
          V  N  T  S  L  R  A  R  Q  A  V  D  H  A  L  R  L  A  P  R
54601 CGCGGGCTCTCCCGGCTGCGCTACCCGTTCTCCGCCGCCCACCACACGGCCACCCCGCCC 54660
          R  G  L  S  R  L  R  Y  P  F  S  A  A  H  H  T  A  T  P  P
54661 CGGACCCTGTCGCTGCTGTGCCCGACCCGCGAACGCGTCGGCAACGTCGAACGCTTCCTC 54720
          R  T  L  S  L  L  C  P  T  R  E  R  V  G  N  V  E  R  F  L
54721 GACAGCGTCGCCCGCACCGCCGCCGCGCCCGGCCGGATAGAGGCCCTCTTCTACGTCGAC 54780
          D  S  V  A  R  T  A  A  A  P  G  R  I  E  A  L  F  Y  V  D
54781 GACGACGACCCCCAACTCCCTGCCTACCACGAGCTGTTCGAGCACGCCCGGTGGCGCTAC 54840
          D  D  D  P  Q  L  P  A  Y  H  E  L  F  E  H  A  R  W  R  Y
54841 GGACGGATCGGCCGGTGCGCCCTGCACGTCGGCGCCCCCGTCGGCGTACCCCACGCCTGG 54900
          G  R  I  G  R  C  A  L  H  V  G  A  P  V  G  V  P  H  A  W
54901 AACCACCTGGCCCGGAACGCGGCCGGCGACGTGCTGATGATGGCCAACGACGACCAGCTC 54960
          N  H  L  A  R  N  A  A  G  D  V  L  M  M  A  N  D  D  Q  L
54961 TACATCGACTACGGCTGGGACACCGCCCTCGACGCCCGCGTCACCGAACTGAGCGCCCTG 55020
          Y  I  D  Y  G  W  D  T  A  L  D  A  R  V  T  E  L  S  A  L
55021 CACCCCGACGGCGTCCTGTGCCTGTACTTCGACGACGGCCAGTACCCCGAGGGCGGCTGC 55080
          H  P  D  G  V  L  C  L  Y  F  D  D  G  Q  Y  P  E  G  G  C
55081 GACTTCCCGATGGTGACACGGCCCTGGTACGGCACCCTCGGCTACTTCACCCCGACGATC 55140
          D  F  P  M  V  T  R  P  W  Y  G  T  L  G  Y  F  T  P  T  I
55141 TTCCAGCAGTGGGAGGTCGAGAAGTGGGTCTTCGACATCGCCGACCGGCTGCACCGGCTC 55200
          F  Q  Q  W  E  V  E  K  W  V  F  D  I  A  D  R  L  H  R  L
55201 TACCCCGTCCCCGGCGTCCTCGTCGAACACCGGCACTACCAGGACTACAAGGCACCCTTC 55260
          Y  P  V  P  G  V  L  V  E  H  R  H  Y  Q  D  Y  K  A  P  F
55261 GACGCCACCTACCAGCGGCACCGGATGACACGGGAGAAGTCCTTCGCCGACCACGCCCTG 55320
          D  A  T  Y  Q  R  H  R  M  T  R  E  K  S  F  A  D  H  A  L
55321 TTCCTGCGCACCGAGCCGGACCGCGAGGCGGAGACGGACAGGCTGCGGGCCGTCATCGCC 55380
          F  L  R  T  E  P  D  R  E  A  E  T  D  R  L  R  A  V  I  A
55381 CGGGCAGGGAACACCCCGGACGCCGACCACGCCGACCATGCCGTTCACGACGCGGAGACC 55440
          R  A  G  N  T  P  D  A  D  H  A  D  H  A  V  H  D  A  E  T
55441 TTCTGGTTCACCGGCCTCCTGCGCGAGTCCCACGCCAAGCTGCTCGCGGAACTCGACGAC 55500
          F  W  F  T  G  L  L  R  E  S  H  A  K  L  L  A  E  L  D  D
55501 GCGCCGGGCCCGGCCGCCGGAGCCGTGCTCTTCGCCGACGGCTCCTGGACCGGCGTCGCC 55560
          A  P  G  P  A  A  G  A  V  L  F  A  D  G  S  W  T  G  V  A
55561 TACCGCACCCACCCGCTGGCCACCGCCCTGCTCGCCTCGATCCCCGAGGCCACCCTCGAC 55620
          Y  R  T  H  P  L  A  T  A  L  L  A  S  I  P  E  A  T  L  D
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55621  TCCGGCCGCGCCGACCTCCTCGTCGTCCCGCCCGGCGCGTCCCACCACCACCCCGACGGC   55680
       S  G  R  A  D  L  L  V  V  P  P  G  A  S  H  H  H  P  D  G

55681  ACCGTCGACTCCGCGTTCGGCTCCGACGCCGGCCTCCGCGTCCTGTTCGGACTGCGCGTG   55740
       T  V  D  S  A  F  G  S  D  A  G  L  R  V  L  F  G  L  R  V

55741  CCGGACGCCGCGCAACTCCGCGTCGGCGACGGCCCGGTGCCCTGGGGCAATGGGCAATGC   55800
       P  D  A  A  Q  L  R  V  G  D  G  P  V  P  W  G  N  G  Q  C

55801  CTGATCCACGACACCGCCGCACCGAGCACCCTGCGCAACGACGGCACCGAATCTCTGGCC   55860
       L  I  H  D  T  A  A  P  S  T  L  R  N  D  G  T  E  S  L  A

55861  GCCCTCACCTTCGTGGTGCCGCGCCCGGCACCGGGGGAGTGAGGCCCGTGTGCGGCATCG   55920
       A  L  T  F  V  V  P  R  P  A  P  G  E  *
                                                M  R  P  V  C  G  I  V   (orf18)

55921  TGGCGATCCGCTCCGCCGACGGCGGACTCGACGGCGGTGAACTCACCGCGCCGATGGCCG   55980
         A  I  R  S  A  D  G  G  L  D  G  G  E  L  T  A  P  M  A  D

55981  ACCTGCGCCCGCGCGGCCCCGACGGCGAAGGCACCTGGGTCTCGCCCACCGGCCGGGCCG   56040
         L  R  P  R  G  P  D  G  E  G  T  W  V  S  P  T  G  R  A  A

56041  CCCTCGGCCACACCCGGCTCGCCGTGATCGCCCCCGACGCCGGACGCCAGCCGGTCGCCG   56100
         L  G  H  T  R  L  A  V  I  A  P  D  A  G  R  Q  P  V  A  G

56101  GCCCGGACGGCACCGTCCGGCTCGTCGTCAACGGCGAGTTCTACGGCTACCGGGAGATCC   56160
         P  D  G  T  V  R  L  V  V  N  G  E  F  Y  G  Y  R  E  I  R

56161  GCGCGGAACTGCGCGCCGcCGGCTGCCGGTTCCGCACCGGCAGCGACAGCGAGATCGCCC   56220
         A  E  L  R  A  A  G  C  R  F  R  T  G  S  D  S  E  I  A  L

56221  TCCACCTGTACCTGCGGGACGGCCGGCGGGCACTGGAGCGGCTGCGCGGCGAGTTCGCCT   56280
         H  L  Y  L  R  D  G  R  R  A  L  E  R  L  R  G  E  F  A  F

56281  TCGTCCTCTGGGACGAACGCCGCGCCACCCTCTTCGCCGCCCGCGACCGGTTCGGCGTCA   56340
         V  L  W  D  E  R  R  A  T  L  F  A  A  R  D  R  F  G  V  K

56341  AACCCCTCTACTACACCGAGCGCGACGGGCGGCTCTACGTCGCCTCGACGGTCAGGGCCC   56400
         P  L  Y  Y  T  E  R  D  G  R  L  Y  V  A  S  T  V  R  A  L

56401  TGCTCTCCTGCGGCGCCCCCGCCCGCTGGGACACCGCCGCCTTCGCCGCGCACCTGCAGC   56460
         L  S  C  G  A  P  A  R  W  D  T  A  A  F  A  A  H  L  Q  L

56461  TCGGCCTGCCCCCCGACCGCACCCTCTTCGCCGGCATCCGGCAGCTCCCGCCCGGCTGCC   56520
         G  L  P  P  D  R  T  L  F  A  G  I  R  Q  L  P  P  G  C  H

56521  ACCTCATCGCCGACGCCCACGGCACCCGCGTCACCCCCTACTGGGACCTCGACTACCCGC   56580
         L  I  A  D  A  H  G  T  R  V  T  P  Y  W  D  L  D  Y  P  P

56581  CCGCCGGCGAACTCGCCGCCCGGGGAAGCCTGGACGACCACCTGGACGCGGTACGCGAAC   56640
         A  G  E  L  A  A  R  G  S  L  D  D  H  L  D  A  V  R  E  R

56641  GGACCGACGAGGCCGTACGGTTGCGTACCGTCGCCGACGTGCCCCTCGCCTGCCACCTCA   56700
         T  D  E  A  V  R  L  R  T  V  A  D  V  P  L  A  C  H  L  S

56701  GCGGCGGCCTGGACTCCTCCGCCGTCGCCGCCTCCGCCGCCCGCCACACCCGGCTCACCG   56760
         G  G  L  D  S  S  A  V  A  A  S  A  A  R  H  T  R  L  T  A

56761  CCTTCACCGTCCGCTTCGACGACCCCGCCTTCGACGAGAGCGCCGTCGCCCGGCGCACCG   56820
         F  T  V  R  F  D  D  P  A  F  D  E  S  A  V  A  R  R  T  A

56821  CCGCCCACCTGGCCATCGACCACCGCGAAGTCGCCTCGGAACGCGCCCACTTCGCGGACC   56880
         A  H  L  A  I  D  H  R  E  V  A  S  E  R  A  H  F  A  D  H

56881  ACCTGCGGGACGTCGTCCGCGCCGGCGAGATGGTGCAGGAGAACTCGCACGGCATCGCCC   56940
         L  R  D  V  V  R  A  G  E  M  V  Q  E  N  S  H  G  I  A  R

56941  GGTACCTGCACAGCGCGCACATCAAGAAGGCGGGATTCACCGCCGTCCTCGCCGGGGAGG   57000
         Y  L  H  S  A  H  I  K  K  A  G  F  T  A  V  L  A  G  E  G

57001  GCGGGGACGAACTGTTCCTCGGCTACCCCCAGTTCCGCAAGGACCTGACGCTCAGCCTGT   57060
         G  D  E  L  F  L  G  Y  P  Q  F  R  K  D  L  T  L  S  L  S
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57061  CCGCCGACGCCCGCGACAAGGCCGACCGCGGCTACGCCCGGCTGGTCGCGGCCGGGCTCC  57120
         A  D  A  R  D  K  A  D  R  G  Y  A  R  L  V  A  A  G  L  L

57121  TGCCGCCGTACCTGCGCACCCTCCTCGGCACCCTCGGCTTCCTGCCCTCCTGGATCGTCG  57180
         P  P  Y  L  R  T  L  L  G  T  L  G  F  L  P  S  W  I  V  D

57181  ACCGCCACCTGGCCGTCACCCAGCCCGTCGCCGCCCTGCTCCGCCCCGACTTCGCCGCCG  57240
         R  H  L  A  V  T  Q  P  V  A  A  L  L  R  P  D  F  A  A  E

57241  AACTGGCCCGCGCCGACGCCGCCGCGCCCCTGCTCGCCGCCGGCGCCGGCCTGCTCGCCG  57300
         L  A  R  A  D  A  A  A  P  L  L  A  A  G  A  G  L  L  A  G

57301  GGCGCGCCCCGGCGCACCAGGCCACCTACCTCTTCGCCAAGACCTGGCTGCCCGGCTACC  57360
         R  A  P  A  H  Q  A  T  Y  L  F  A  K  T  W  L  P  G  Y  L

57361  TGCTCGCCGCCGAACGCCTCGACGCGGCCCAGGCCGTCGAGGTGCGGCTGCCCCTCTTCG  57420
         L  A  A  E  R  L  D  A  A  Q  A  V  E  V  R  L  P  L  F  D

57421  ACCACCACCTCTTCGACCTCGTCCGGCACACCCCGCCGGCCTGGTACGACAAGGACGGCA  57480
         H  H  L  F  D  L  V  R  H  T  P  P  A  W  Y  D  K  D  G  T

57481  CCGGCAAGTACCCGCTGCGGGCCGCCATGCGCCACCGGCTGCCGCGCGAGGTGACCGAGG  57540
         G  K  Y  P  L  R  A  A  M  R  H  R  L  P  R  E  V  T  E  G

57541  GCCGCAAACAGGGCTTCCTCGCACCTCCGATGGCCGACGACGACACCCTCCTCGACGCCC  57600
         R  K  Q  G  F  L  A  P  P  M  A  D  D  D  T  L  L  D  A  L

57601  TGCGCGAACGCCTCGCCGGACCGGGCGCGGGCGACGACCCCTTCTTCGACCCGCACGCCG  57660
         R  E  R  L  A  G  P  G  A  G  D  D  P  F  F  D  P  H  A  V

57661  TCCGCGCCCTGCTGGACCGGCTGGCCGCCGCACCCCCGGGGCAGCGGTCCGGCGGCGAGA  57720
         R  A  L  L  D  R  L  A  A  A  P  P  G  Q  R  S  G  G  E  K

57721  AACTCCTCCAACTCGTCGCGAGCACCGCCGAACTGGCCGACGAGTTCGGCCTCACCACCG  57780
         L  L  Q  L  V  A  S  T  A  E  L  A  D  E  F  G  L  T  T  A

57781  CCCCCAGCGGGCAGAAAGGCGGCAACGGTGGCTGACCTCGATCCCGGCACGCTCTCCGAG  57840
         P  S  G  Q  K  G  G  N  G  G  *

57841  GCCGAGCTGACCGCCCGGATCGCCGCCCTGTCCCCCGAACGCCGGGCGGCGTTCGAGAAG  57900

57901  ATGCTGCACGGCGCCGCGCACCCCCGCCCCGGCATCCCGCGCCGCGGCGCCACCGCGGCA  57960
         M  L  H  G  A  A  H  P  R  P  G  I  P  R  R  G  A  T  A  A    (orf17)

57961  CCGGCCTCCTACGGCCAGGAACGCCTGTGGCTGCTCACCGGGCTGCTGCCCACCGCCTAC  58020
         P  A  S  Y  G  Q  E  R  L  W  L  L  T  G  L  L  P  T  A  Y

58021  AACTACGCCACCGCCCTGCGGCTGCGCGGCGACCTGTCCGTCCCCGCGCTGCGCGGCGCC  58080
         N  Y  A  T  A  L  R  L  R  G  D  L  S  V  P  A  L  R  G  A

58081  CTGCGCGGCATCGTCCGCCGCCACGAGGTGCTGCGCACCACCTTCCGGCTGGACGGCGAC  58140
         L  R  G  I  V  R  R  H  E  V  L  R  T  T  F  R  L  D  G  D

58141  GACCTCATCCAGGTCGTCCACCCCACGGCGGACGTCCCCGTGCGCCTGGCCGACCTCACC  58200
         D  L  I  Q  V  V  H  P  T  A  D  V  P  V  R  L  A  D  L  T

58201  GGACGCTCCGCCGACACCGGGCGGCTGATGCGCGAGGAGGCCCGCCGCCCCTTCGACCTG  58260
         G  R  S  A  D  T  G  R  L  M  R  E  E  A  R  R  P  F  D  L

58261  GAGCACGGGCCGCTGCTGCGGCTGACCCTCTTCCGGCTCGGCCCCCGCGACCACCTCGCC  58320
         E  H  G  P  L  L  R  L  T  L  F  R  L  G  P  R  D  H  L  A

58321  CTGCTGGCCGTCCACCACGCCGTCACCGACGGCTGGTCCAACGGCGTCCTCGTGACCGAA  58380
         L  L  A  V  H  H  A  V  T  D  G  W  S  N  G  V  L  V  T  E

58381  CTCGCCACCGGCTACCGGGAACTGCGCGCCGGACGCCCCGACCGGCGGCCCGCCCCGCCG  58440
         L  A  T  G  Y  R  E  L  R  A  G  R  P  D  R  R  P  A  P  P

58441  GTCCAGTACGGCGACTACGCGCACTGGCAGCGCGAGCGGCTGACCGGGCCCGAACTGCGG  58500
         V  Q  Y  G  D  Y  A  H  W  Q  R  E  R  L  T  G  P  E  L  R

58501  GCCCTGGAGGACTACTGGCGCACCGCCGTACGCGACCTGCCCAGGACGGACCTGCCCACC  58560
         A  L  E  D  Y  W  R  T  A  V  R  D  L  P  R  T  D  L  P  T
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58561 GACCGCCCCCGCCCCGCCGCCCGGCGCGGCGAGGGCGCCAACCACGCCCTGCTGCTCTCG 58620
D R P R P A A R R G E G A N H A L L L S

58621 CCGGAGCTGACCGGCCGGCTCGCCGACCTGCGCCGCCGCGAGGGCGGGTCGCTGTTCATG 58680
P E L T G R L A D L R R R E G G S L F M

58681 CTCGTGCTCTCCGCGCTCCTGGTCGTCCTGCGTGGCACCGGCGGCCGGGACCGGCTCGCC 58740
L V L S A L L V V L R G T G G R D R L A

58741 GTCGGCACCCTCGTCGCCGGCCGCACCCGCCCCGAACTCGAGCCGCTCATCGGCTACTTC 58800
V G T L V A G R T R P E L E P L I G Y F

58801 GTCAACGTCCTGCTGCTGCCCTTCGAGACCGGCGGCCGGACCTCCTTCGCCGAGCTGTGG 58860
V N V L L L P F E T G G R T S F A E L W

58861 CGGCGGGTCCGCGGCCGGCTGGTGGAGGCGTACGCCCACCAGGAACTGCCGCTGGAGAAG 58920
R R V R G R L V E A Y A H Q E L P L E K

58921 GCCCTGGAGCTGCTGCGCGCCGACGGCACCGCCCCCGCCGACCCGCCGGTCGGCGTGGTC 58980
A L E L L R A D G T A P A D P P V G V V

58981 TGCGTCGCCCAGCAGCCCGCCCCCGCGATCACCCTGCCCGGACTCGACGCGAGCGTCGAG 59040
C V A Q Q P A P A I T L P G L D A S V E

59041 GACGTCGACCTGGGCACCGCCCAGTTCGACCTCGTCGTCGAGGTGCGCGAACGGCCGGAA 59100
D V D L G T A Q F D L V V E V R E R P E

59101 GGCGTGCAGATCGCCTTCCAGTACGACCGGGACCTGTTCGACGCGGCCACGGTCCGGCTC 59160
G V Q I A F Q Y D R D L F D A A T V R L

59161 CTCGCCGACCACGTGCACGCCGTCCTCGACCAGGCCGCCGCCGACCCCACCCTGCCCTGT 59220
L A D H V H A V L D Q A A A D P T L P C

59221 GCCGAGCTGCCCGCCCCGCCGGCCCCCGCGGCCCCGGCCCGCACGGCCGGCGCCACGACG 59280
A E L P A P P A P A A P A R T A G A T T

59281 CTGCACGCCCTGTTCGAGTCCCGCGCCGCGAAGAGCCCCGACGCGGTCGCCCTCGTCGAC 59340
L H A L F E S R A A K S P D A V A L V D

59341 GGCGGCCACCGCGTCACCTACCGGACCCTCAACACCCGCGCCAACCGGCTCGCCCGCCAC 59400
G G H R V T Y R T L N T R A N R L A R H

59401 CTGCGCGCGGTCGGCGTGCGTACCGAGGACCGGGTGGCGCTGCGCCTGCCCCGCGGCACC 59460
L R A V G V R T E D R V A L R L P R G T

59461 GACGCGGTGACCGCCACCCTCGCCGCCCTCAAGGCCGGCGCCGCGTACGTACCCCTCGAC 59520
D A V T A T L A A L K A G A A Y V P L D

59521 CCCGCCCTCCCCGAGGAACGGCTGACCCGCGTCCTCGCCGACGCCCGCCCCGCCGTGGTC 59580
P A L P E E R L T R V L A D A R P A V V

59581 CTCACCCCCGCGTATCTGCACGACCGGTCCGCCGAGATCACCGCCCACGCCGGCCATGAC 59640
L T P A Y L H D R S A E I T A H A G H D

59641 CTCAACCTCCCCGTCCACCCCGACAACCTCGCCTACCTCCTCCACACCTCCGGATCCACC 59700
L N L P V H P D N L A Y L L H T S G S T

59701 GGCACCCCCaAGGGCGTCCTCGGCAcCCACCGGGGCGCGGTCAACCGCGTCGACTGGATG 59760
G T P K G V L G T H R G A V N R V D W M

59761 AGCACCGCGTACCCGTTCCGGACCGGCGACGTGGCCGTCGCCCGCACCGCGCCCGGCTTC 59820
S T A Y P F R T G D V A V A R T A P G F

59821 GTCGACGCGGTCTGGGAACTCTTCGGCCCCCTGGCCGCCGGCGTCCCCCTCGTCCTCCTG 59880
V D A V W E L F G P L A A G V P L V L L

59881 CCGACCGACGAGGCGCGCGACCCGGCCCTGCTGACGGCGGCGCTGGAACGGCACCGGGTG 59940
P T D E A R D P A L L T A A L E R H R V

59941 AGCCGGATGGTGACGGTCCCGTCGCTGCTGACCATGCTCCTGGACGAGTCCGCCCGCGCG 60000
S R M V T V P S L L T M L L D E S A R A

60001 ACGGACCTCGGCACCCGCCTGGCCTGCCTCCGCACCTGGATCACCAGCGGCGAGCCCCTG 60060
T D L G T R L A C L R T W I T S G E P L

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60061  CCGCCCGCGCTCGCCCGGCGGTTCCACGACCGCCTGCCCGGCCGCACCCTGCTGAACCTG  60120
       P  P  A  L  A  R  R  F  H  D  R  L  P  G  R  T  L  L  N  L

60121  TACGGCTCCTCCGAGACCGCCGCCGACGCCACCGCGGCCCGCATCGACCCGGCGCCCGGG  60180
       Y  G  S  S  E  T  A  A  D  A  T  A  A  R  I  D  P  A  P  G

60181  ACTGCGCTCCCGGAGCGGTCCCCGATCGGCACGCCCATCACCGGCGTCAGCGCCCTCGTC  60240
       T  A  L  P  E  R  S  P  I  G  T  P  I  T  G  V  S  A  L  V

60241  CGCGGCCCGGACCTGCGCCCGCTGCCCGCGCTGATGCCCGGCGAGCTGTACGCCGGGGGC  60300
       R  G  P  D  L  R  P  L  P  A  L  M  P  G  E  L  Y  A  G  G

60301  GCGTGCGTGGCCCGCGGCTACCACGCCCGTCCGGCCGAGACCGCCGCGGCGTTCCCGCCG  60360
       A  C  V  A  R  G  Y  H  A  R  P  A  E  T  A  A  A  F  P  P

60361  GATCCCGACGGCGGGCCCGGCGCCCGGATGTTCCGTACCGGTGACAGGGCCCGGCTGCGG  60420
       D  P  D  G  G  P  G  A  R  M  F  R  T  G  D  R  A  R  L  R

60421  GCCGACGGCCGGCTGGAACTCCTGGGGCGCGTGGACCGGCAGGTGCAGATCCGCGGCCAG  60480
       A  D  G  R  L  E  L  L  G  R  V  D  R  Q  V  Q  I  R  G  Q

60481  CGCGCCGAGCCCGGCGAGGTCGAACACGCCCTGCTGGCCCACCCGGCCGTACGGGCCGCC  60540
       R  A  E  P  G  E  V  E  H  A  L  L  A  H  P  A  V  R  A  A

60541  GCCGTCACGGCGAACCCCGACGCCACCGGCCTGTGGGCGTACGTGCGGCTCGCTCCCGGC  60600
       A  V  T  A  N  P  D  A  T  G  L  W  A  Y  V  R  L  A  P  G

60601  CCGTTCGCCGCCGGCTCCCCCCAGACCGAGCTGACCGCCTTCCTGCGCCGCACGCTCCCT  60660
       P  F  A  A  G  S  P  Q  T  E  L  T  A  F  L  R  R  T  L  P

60661  GCCCACCTCGTGCCCACCGCCGTCACCGTCCTGGACGAGCTGCCGGTGACCGCGCACGGC  60720
       A  H  L  V  P  T  A  V  T  V  L  D  E  L  P  V  T  A  H  G

60721  AAGACCGACCACGCGCGGCTGCCCGCCCCCGACCCCCGGGCCGGGCGCCCCGCCCCGACC  60780
       K  T  D  H  A  R  L  P  A  P  D  P  R  A  G  R  P  A  P  T

60781  GCCCCCCGCACCCCCACCGAGCGTACGGTCGCCGACGTCTTCGCCGGGGTGCTCGGCCTG  60840
       A  P  R  T  P  T  E  R  T  V  A  D  V  F  A  G  V  L  G  L

60841  GAGGGGCCGGTCGGCGCGCACGACGACTTCTTCCTCCTCGGCGGGCACTCCCTCCTCGCC  60900
       E  G  P  V  G  A  H  D  D  F  F  L  L  G  G  H  S  L  L  A

60901  GCCCGCAGTCGCGGCGGAACTCCGCGCCCGCCGCGGCGTCCGGATCGGGCTGAGCGACGT  60960
       A  R  S  R  G  G  T  P  R  P  P  R  R  P  D  R  A  E  R  R

60961  CTTCGCGGCCCCCACCGTCGCCGCAGCGTCGCCGCCCGGACCGACGCCGCCCGGCCCGGC  61020
       L  R  G  P  H  R  R  R  S  V  A  A  R  T  D  A  A  R  P  G

61021  ACCGGCCCCGAGCACACCCCGTTCGTCACCGACCCCGGCGCCCGGCACGAGCCGTTCCCG  61080
       T  G  P  E  H  T  P  F  V  T  D  P  G  A  R  H  E  P  F  P

61081  CTCACCGACGTCCAGCGGGCCTACTACGTGGGACGCGAGGGCGGGTTCGCCCTCGGCGGC  61140
       L  T  D  V  Q  R  A  Y  Y  V  G  R  E  G  G  F  A  L  G  G

61141  GTCTCCACCCACGCCTACCTGGAGATCGAGGCCCCGCGGATCGACGTCGCACGGTTTACC  61200
       V  S  T  H  A  Y  L  E  I  E  A  P  R  I  D  V  A  R  F  T

61201  GGCGCGCTGCGCGGGGTGATCGCCCGGCACCCCATGCTGCGCGCCGTGATCCGTCCCGAC  61260
       G  A  L  R  G  V  I  A  R  H  P  M  L  R  A  V  I  R  P  D

61261  GGGCTCCAGCAGGTGCTCACCGACGTCCCCCCGTACGACGTGGCCGTGCACGACCTGCGC  61320
       G  L  Q  Q  V  L  T  D  V  P  P  Y  D  V  A  V  H  D  L  R

61321  GACCTGGACGAGCCCGCGCGGCAGCGCCGACGCGCCGCGCTGCGCGAGGAGATGTCCCAC  61380
       D  L  D  E  P  A  R  Q  R  R  R  A  A  L  R  E  E  M  S  H

61381  CAGGTGGTGCCCGCCGACCTCTGGCCCCTGTTCGACGTCCGCGTCTCCCTCGGCCCCACG  61440
       Q  V  V  P  A  D  L  W  P  L  F  D  V  R  V  S  L  G  P  T

61441  GACGCCCTCGTCCACGTGGGGGTGGACGCGCTGATCTGCGACGCCCACAGCTTCGGCCTC  61500
       D  A  L  V  H  V  G  V  D  A  L  I  C  D  A  H  S  F  G  L

61501  GTCCTGGCCGAACTCGCGGCCCGTTACGCCGACCCCGCACGCCGCTTCCCGCCCCTGACG  61560
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        V  L  A  E  L  A  A  R  Y  A  D  P  A  R  R  F  P  P  L  T
        .     .     .     .     .     .     .     .     .     .
61561   GCGGACTTCCGGGACCACGTCCTCCATCAGGAGGCGCTCCGCGGAACCGCCGAGTACGCG   61620
        A  D  F  R  D  H  V  L  H  Q  E  A  L  R  G  T  A  E  Y  A
        .     .     .     .     .     .     .     .     .     .
61621   GCGGCGGAGCGGTACTGGCGCGAACGCCTGCCCGAGCTGCCGCCCGGCCCCGAACTGCCC   61680
        A  A  E  R  Y  W  R  E  R  L  P  E  L  P  P  G  P  E  L  P
        .     .     .     .     .     .     .     .     .     .
61681   CTGGCCGTCGCGCCCGAGACCCTCGGCACCCCGCGCTTCACCCGCCGCTCCGGCCGGCTG   61740
        L  A  V  A  P  E  T  L  G  T  P  R  F  T  R  R  S  G  R  L
        .     .     .     .     .     .     .     .     .     .
61741   GACGCGGCCTCCTGGACGGCGGTCAAGGACCGGGCCCGCCGCGCCGGGCTCAGCCCCTCC   61800
        D  A  A  S  W  T  A  V  K  D  R  A  R  R  A  G  L  S  P  S
        .     .     .     .     .     .     .     .     .     .
61801   GGCGTACTGCTGGCGGCGTTCGCCGAGGTGATCACCGCGTGGAGCGGCCGGCCGCGCTAC   61860
        G  V  L  L  A  A  F  A  E  V  I  T  A  W  S  G  R  P  R  Y
        .     .     .     .     .     .     .     .     .     .
61861   TCGCTGATGCTGACGGTCTTCGACCGCCCGCCGCTCCACCCGGACCTCGGGCGGATCGTC   61920
        S  L  M  L  T  V  F  D  R  P  P  L  H  P  D  L  G  R  I  V
        .     .     .     .     .     .     .     .     .     .
61921   GGCGACTTCACCTCGCTCAGCCTGCTGGAGGTCGACCACAGTCGGCCCGGCGACTTCACC   61980
        G  D  F  T  S  L  S  L  L  E  V  D  H  S  R  P  G  D  F  T
        .     .     .     .     .     .     .     .     .     .
61981   GACAGGGCCCGCGCCCTCCAGCGCCGCCTGTGGCAGGACCTCGACCACCTGGCGGTCGGC   62040
        D  R  A  R  A  L  Q  R  R  L  W  Q  D  L  D  H  L  A  V  G
        .     .     .     .     .     .     .     .     .     .
62041   GGCGTGACGGTGACACGGGAACGGGCGCTGCGCCACGACGCCCGACCCGGTCTGCTCACA   62100
        G  V  T  V  T  R  E  R  A  L  R  H  D  A  R  P  G  L  L  T
        .     .     .     .     .     .     .     .     .     .
62101   CCCGTCGTCTTCACCTCCGACCTGCCTGTCGGCGAGACCGCGGCCGAGGACGCGGACGGG   62160
        P  V  V  F  T  S  D  L  P  V  G  E  T  A  A  E  D  A  D  G
        .     .     .     .     .     .     .     .     .     .
62161   GGAGAGGGATGGGCGCTCGGAGAGCCCGTCTACGGCGTCAGCCAGACCCCGCAGGTCCAT   62220
        G  E  G  W  A  L  G  E  P  V  Y  G  V  S  Q  T  P  Q  V  H
        .     .     .     .     .     .     .     .     .     .
62221   CTCGACCATCAAGTCGCCGAAGACCGAGGGGAGTTGGTCTTCAACTGGGACGCCGTGGAA   62280
        L  D  H  Q  V  A  E  D  R  G  E  L  V  F  N  W  D  A  V  E
        .     .     .     .     .     .     .     .     .     .
62281   GACCTGTTCGCCCCGGGCGCCCTGGACGCCATGTTCGCCGCCTACACCGCCTCGCTGACC   62340
        D  L  F  A  P  G  A  L  D  A  M  F  A  A  Y  T  A  S  L  T
        .     .     .     .     .     .     .     .     .     .
62341   CGCCTGGCCCGGAGCCCCGAAGCCTGGCGGCGGCCCGGCACGCCGCCGCTGCCCACCGCC   62400
        R  L  A  R  S  P  E  A  W  R  R  P  G  T  P  P  L  P  T  A
        .     .     .     .     .     .     .     .     .     .
62401   CAGGCGGCCGTGCGCCGGCGCACCGCCGCGACCGAGGCGCCCCTGCCCGCCCGCCTGCTG   62460
        Q  A  A  V  R  R  R  T  A  A  T  E  A  P  L  P  A  R  L  L
        .     .     .     .     .     .     .     .     .     .
62461   CACGAGGCCGTCGGCGACGCGGCCCGGCGCCACGCCGACCTGACCGCCCTGGTCGACGGC   62520
        H  E  A  V  G  D  A  A  R  R  H  A  D  L  T  A  L  V  D  G
        .     .     .     .     .     .     .     .     .     .
62521   GACACCCGGATGACCTACCGGCGACTGACCGAGCACGCCCGGCGCGTCGGCCGCACGCTG   62580
        D  T  R  M  T  Y  R  R  L  T  E  H  A  R  R  V  G  R  T  L
        .     .     .     .     .     .     .     .     .     .
62581   CGCCGCCTCGGCGCCCGCCCCGGCCGCCTGGTCCCGGTGGTCGCCCGCAAGGGGTGGCGG   62640
        R  R  L  G  A  R  P  G  R  L  V  P  V  V  A  R  K  G  W  R
        .     .     .     .     .     .     .     .     .     .
62641   CAGGCCGTCGCCGCGCTGGGCGTCCTGGAGTCGGGGGCGGCGTACCTGCCCCTGGACCCC   62700
        Q  A  V  A  A  L  G  V  L  E  S  G  A  A  Y  L  P  L  D  P
        .     .     .     .     .     .     .     .     .     .
62701   GAACTGCCCGCCGAACGGCTCGTCCACCTCGTACGGCGCGCCGAAGCCGCCCTCCTCCTC   62760
        E  L  P  A  E  R  L  V  H  L  V  R  R  A  E  A  A  L  L  L
        .     .     .     .     .     .     .     .     .     .
62761   ACCGAACGCGCCCTGCTGGACACGCTCGCCGTCCCCGTCGGCGTCACCGTGCTCGCGGTG   62820
        T  E  R  A  L  L  D  T  L  A  V  P  V  G  V  T  V  L  A  V
        .     .     .     .     .     .     .     .     .     .
62821   GACGACGACGCGGCCCTCGACGCCGACGGCGGCCCGCTGCAGAGCGTGCAGAACCTCACC   62880
        D  D  D  A  A  L  D  A  D  G  G  P  L  Q  S  V  Q  N  L  T
        .     .     .     .     .     .     .     .     .     .
62881   GACCTGGCGTACACCATCTTCACCTCGGGCTCCACCGGCGAACCCAAGGGCGTCATGATC   62940
        D  L  A  Y  T  I  F  T  S  G  S  T  G  E  P  K  G  V  M  I
        .     .     .     .     .     .     .     .     .     .
62941   GACCACCTCGGCGCGGCCAACACCCTGGAATGCGTCAACCGCCGCTTCGGCACCGGCCCC   63000
        D  H  L  G  A  A  N  T  L  E  C  V  N  R  R  F  G  T  G  P
        .     .     .     .     .     .
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63001  GGCGACGCGGTCCTCGCCGTCTCCTCCCCGAGCTTCGACCTCGCCGTCTACGACCTGTTC  63060
       G  D  A  V  L  A  V  S  S  P  S  F  D  L  A  V  Y  D  L  F
                .     .     .     .     .     .     .     .     .
63061  GGCGTGCTGGCCGCCGGCGGCACCGTGGTCGTCCCCGCCCACGACCGCCGGCGCGACCCC  63120
       G  V  L  A  A  G  G  T  V  V  V  P  A  H  D  R  R  R  D  P
                .     .     .     .     .     .     .     .     .
63121  GGACACTGGGCCGAGCTGATCCGGCGCGAGCGGGTCACCCTGTGGAACTCCGTCCCCGCG  63180
       G  H  W  A  E  L  I  R  R  E  R  V  T  L  W  N  S  V  P  A
                .     .     .     .     .     .     .     .     .
63181  CTGGGCACCCTGCTCACCGAGTACGCCGAGGCCCTCGCCCCCGACGCCCTGCGCACCCTG  63240
       L  G  T  L  L  T  E  Y  A  E  A  L  A  P  D  A  L  R  T  L
                .     .     .     .     .     .     .     .     .
63241  CGGGCGGTGCTCCTCAGCGGCGACTGGATCCccctcggactgcccgaccGGATCCGCGCC  63300
       R  A  V  L  L  S  G  D  W  I  P  L  G  L  P  D  R  I  R  A
                .     .     .     .     .     .     .     .     .
63301  CTGTCCGCCCCCGGCGCCACCGTGATGAGCCTCGGCGGCGCGACCGAAGCCTCCATCTGG  63360
       L  S  A  P  G  A  T  V  M  S  L  G  G  A  T  E  A  S  I  W
                .     .     .     .     .     .     .     .     .
63361  TCGGTCTGGTACGAGATCGGGAAGGTGCACGAGGCGTGGAGCAGCATCCCCTACGGCACC  63420
       S  V  W  Y  E  I  G  K  V  H  E  A  W  S  S  I  P  Y  G  T
                .     .     .     .     .     .     .     .     .
63421  CCCATGGCCAACCAGCGGCTGGAGGTCCTCGACGAGCAGCTGCGGCCCCGGCCCGACTGG  63480
       P  M  A  N  Q  R  L  E  V  L  D  E  Q  L  R  P  R  P  D  W
                .     .     .     .     .     .     .     .     .
63481  GTGCCCGGCGAGCTGTACATCGGCGGCACCGGCGTCGCCAAGGGCTACTGGCGCGACCCG  63540
       V  P  G  E  L  Y  I  G  G  T  G  V  A  K  G  Y  W  R  D  P
                .     .     .     .     .     .     .     .     .
63541  GAACAGACCTCCCTGCGCTTCCCCGTCCACCCGGGCAGCGGGCAACGCCTGTACCGCACC  63600
       E  Q  T  S  L  R  F  P  V  H  P  G  S  G  Q  R  L  Y  R  T
                .     .     .     .     .     .     .     .     .
63601  GGGGACTTCGCCCGCCACCTCCCCGACGGCACGCTGGAATTCCTGGGCCGGCAGGACGAC  63660
       G  D  F  A  R  H  L  P  D  G  T  L  E  F  L  G  R  Q  D  D
                .     .     .     .     .     .     .     .     .
63661  CAGGTGAAGATCGGCGGATTCCGGGTCGAACTGGGCGAGGTCGAGGCGGCCCTCGGCCGA  63720
       Q  V  K  I  G  G  F  R  V  E  L  G  E  V  E  A  A  L  G  R
                .     .     .     .     .     .     .     .     .
63721  CTGCCCGACGTCGCCGCCGGCGCGGTGATCGCCACCGGTGACCCGCGGGGCGACCGCCGC  63780
       L  P  D  V  A  A  G  A  V  I  A  T  G  D  P  R  G  D  R  R
                .     .     .     .     .     .     .     .     .
63781  CTCGTCGGCTTCGCCGTACCGGCCCGGGAGGGCGGCTTCGACGCGGCCGGGCTCCGACGG  63840
       L  V  G  F  A  V  P  A  R  E  G  G  F  D  A  A  G  L  R  R
                .     .     .     .     .     .     .     .     .
63841  CAACTCGCCCGGCGGCTGCCCGCCTACATGGTCCCCACGACCCTGCTGCCCCTGGACCGG  63900
       Q  L  A  R  R  L  P  A  Y  M  V  P  T  T  L  L  P  L  D  R
                .     .     .     .     .     .     .     .     .
63901  CTGCCGCTGACCGCCAACGGCAAGGTCGACCGGGCCGCACTCCAACGCCTCGTCCCCGGC  63960
       L  P  L  T  A  N  G  K  V  D  R  A  A  L  Q  R  L  V  P  G
                .     .     .     .     .     .     .     .     .
63961  CGCGCACCGGCCCCGGCGGAACCCGCCACCGCCCCACCTGCCCGTTCCCGCGCCGTCCCC  64020
       R  A  P  A  P  A  E  P  A  T  A  P  P  A  R  S  R  A  V  P
                .     .     .     .     .     .     .     .     .
64021  GTGCCCGGCTGGCTCGCCGACCTGTGGTGCGAACTCCTCGACGTGCCGGAGGCCGACCCC  64080
       V  P  G  W  L  A  D  L  W  C  E  L  L  D  V  P  E  A  D  P
                .     .     .     .     .     .     .     .     .
64081  GACGCGAACTTCTTCGCCCTCGGCGGCACCTCCCGGGTCGCGATCACCCTGGTCACCCGG  64140
       D  A  N  F  F  A  L  G  G  T  S  R  V  A  I  T  L  V  T  R
                .     .     .     .     .     .     .     .     .
64141  ATCGAGGCCCGACTCGCCGTCCGGGTGCCCCTCGCCCGCCTCTTCGACGCCCGCACCCTG  64200
       I  E  A  R  L  A  V  R  V  P  L  A  R  L  F  D  A  R  T  L
                .     .     .     .     .     .     .     .     .
64201  GGCGGCCTCGCCGAGACGATCGCCGAACTGTCGGCCGCCGCCGAGGAGGAGCCGGCACCC  64260
       G  G  L  A  E  T  I  A  E  L  S  A  A  A  E  E  E  P  A  P
                .     .     .     .     .     .     .     .     .
64261  GCCGAGCCCGTGTACGCCCCCGACCCCGCCACCCGCCACGAGCCGTTCCCGCTCACCGAC  64320
       A  E  P  V  Y  A  P  D  P  A  T  R  H  E  P  F  P  L  T  D
                .     .     .     .     .     .     .     .     .
64321  ATCCAGCGCGCCTACTGGCTCGGCCGGCACCGCTCCCTCTCCCTTGGCGGCGTCGCCACG  64380
       I  Q  R  A  Y  W  L  G  R  H  R  S  L  S  L  G  G  V  A  T
                .     .     .     .     .     .     .     .     .
64381  CACACCTACCTCGAACTCGACGTCGAGGACCTCGACCCCGGCCGGCTCCAGACGGCCCTC  64440
       H  T  Y  L  E  L  D  V  E  D  L  D  P  G  R  L  Q  T  A  L
                .     .     .     .     .     .     .     .     .
64441  CGCCGGCTGATCGACCGCCACGACGCCCTCCGGCTCGTGGTCCTCCCCGACGGCCGGCAA  64500
       R  R  L  I  D  R  H  D  A  L  R  L  V  V  L  P  D  G  R  Q
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64501  CAGATCCTCGGCGACGTACCGCCGTACCTCCTCGCCCACACCGACCTGCGGGGCAGGGCG  64560
       Q  I  L  G  D  V  P  P  Y  L  L  A  H  T  D  L  R  G  R  A

64561  GACGCCGAGGCCGAACTGGCCCGCGTCCGCGAGCACATGTCGCACGAGGTGCGCGACGCC  64620
       D  A  E  A  E  L  A  R  V  R  E  H  M  S  H  E  V  R  D  A

64621  TCCCGCTGGCCGCTGTTCGACGTACGGACCCACCGCCTGGACGACGTCCGCACCCGGCTG  64680
       S  R  W  P  L  F  D  V  R  T  H  R  L  D  D  V  R  T  R  L

64681  CACCTGAGCTTGGACCTGCTCATCGCCGACGCCCACAGCGTCCACGTACTCACCGGCGAC  64740
       H  L  S  L  D  L  L  I  A  D  A  H  S  V  H  V  L  T  G  D

64741  CTGCTCACCTTCTACGCCGACCCCGACGCGGCCCTGCCGCCCCTCGGCTGCTCCTTCCGC  64800
       L  L  T  F  Y  A  D  P  D  A  A  L  P  P  L  G  C  S  F  R

64801  GACTACGTCCTGGCCGTCCGCGCCCACGCCGAGGGCGAGCCGCGCCGCCGCGCCCTCGAC  64860
       D  Y  V  L  A  V  R  A  H  A  E  G  E  P  R  R  R  A  L  D

64861  CACTGGCGGGCCCGGCTGGCCGACCTGCCGGGCCCGCCCGGCCTGCCGCTGCGGTGCCGG  64920
       H  W  R  A  R  L  A  D  L  P  G  P  P  G  L  P  L  R  C  R

64921  CCCGAGGAGCTGACCGCGCCGCGGTTCGCCCGCCTCACCACCGGACTCGGCCCCGACGCC  64980
       P  E  E  L  T  A  P  R  F  A  R  L  T  T  G  L  G  P  D  A

64981  TGGGCACGGCTGCGGCGCGCCGCGGCGGCCGCCGAACTCACCCCGGCCGCACTGATCTGC  65040
       W  A  R  L  R  R  A  A  A  A  A  E  L  T  P  A  A  L  I  C

65041  GCCGCCTTCTGCGACGTCCTCGCCCAGTGGAGCGACACCCCCCGCTTCACCCTCAACCTC  65100
       A  A  F  C  D  V  L  A  Q  W  S  D  T  P  R  F  T  L  N  L

65101  ACCACCTTCCACCGCCCCGCCCTGCTCCCCGGCGTGGACGACCTCGTCGGCGACTTCACC  65160
       T  T  F  H  R  P  A  L  L  P  G  V  D  D  L  V  G  D  F  T

65161  ACCACGACCCTGCTCGGGGTCGACGGCGAGGGGGACACCTTCCGGGACCGGGCCCGCCGA  65220
       T  T  T  L  L  G  V  D  G  E  G  D  T  F  R  D  R  A  R  R

65221  CTCCAGGACCGCATCTGGGAGGACCTCGAACACCGCGTCGTCAGCGGCGTCGAGGTCCTG  65280
       L  Q  D  R  I  W  E  D  L  E  H  R  V  V  S  G  V  E  V  L

65281  CGGATGCTGCGCCGCGAGCGGGGCACCCACGACGCCGTCCGGATGCCGGTCGTCTTCACC  65340
       R  M  L  R  R  E  R  G  T  H  D  A  V  R  M  P  V  V  F  T

65341  AGCACCCTGCGGGCCGCCGGCCCCGCCCCCCGGACGGCCCCGCCCGCCTGGCGGGTACGG  65400
       S  T  L  R  A  A  G  P  A  P  R  T  A  P  P  A  W  R  V  R

65401  CCCGGCTACGCGATCAGCCAGACCCCGCAGGTCCTGCTCGACCATCAGGTGAGCGAGAGC  65460
       P  G  Y  A  I  S  Q  T  P  Q  V  L  L  D  H  Q  V  S  E  S

65461  GACGGCCGACTGGTCTGCACCTGGGACTACGTCGCGGACGCCTACCCGCCCGGGCTGATC  65520
       D  G  R  L  V  C  T  W  D  Y  V  A  D  A  Y  P  P  G  L  I

65521  GAGGCCATGTTCGGGGCCTTCGAGGCGCTCCTCGCCTCGCTCGCCGGTCACGACGACGAC  65580
       E  A  M  F  G  A  F  E  A  L  L  A  S  L  A  G  H  D  D  D

65581  GCCGGCCACGACGACGACGCCGGCCACGACGACGGCCCCGGCCACGACGACGGCCCCGGC  65640
       A  G  H  D  D  D  A  G  H  D  D  G  P  G  H  D  D  G  P  G

65641  CACGACGACGGCCCCGGCCACGACGACGGCCCCGGCCACGACGACGGCCCCGGCCGCGAC  65700
       H  D  D  G  P  G  H  D  D  G  P  G  H  D  D  G  P  G  R  D

65701  GACAGTGCCGATCACGGCCACAGTGCCACGCACGACGACAGCGCCGCCCGAAACGACAGA  65760
       D  S  A  D  H  G  H  S  A  T  H  D  D  S  A  A  R  N  D  R

65761  GAGGGAGGTGGACCGGAGTGACGAGCGCCCGGCCCACGCCGACACTGCTCCCCGCCGACC  65820
       E  G  G  G  P  E  *
                         M  T  S  A  R  P  T  P  T  L  L  P  A  D  Q  (orf16)

65821  AGCGGGAGCTGCTGCGGATGATGAACGACCGCACCGCACCCGTGCCCGCGCACACCCTCA  65880
         R  E  L  L  R  M  M  N  D  R  T  A  P  V  P  A  H  T  L  T

65881  CCGCCCAACTGGCCGACGCCGCGCGCACGCACGACCGGGCTCTGGCACTGGTGGCACCGG  65940
         A  Q  L  A  D  A  A  R  T  H  D  R  A  L  A  L  V  A  P  G
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65941  GTCTGACACTGAGCCACGCCGAACTGGACGCCCGGGCGGCCGCGGTGGCCGCCCGGCTCA  66000
        L  T  L  S  H  A  E  L  D  A  R  A  A  A  V  A  A  R  L  T

66001  CCGCCGCGGGCGTCATCCCCGGGGACCGGGTCGCCCTCGCCGTCGAGTACGGCTGGGAGC  66060
        A  A  G  V  I  P  G  D  R  V  A  L  A  V  E  Y  G  W  E  Q

66061  AGGTCGTGGGCGCCCTGGCCGCGCTCCGCGCCGGAGCCGTCTGCCTGCCCGTCGCCCCCG  66120
        V  V  G  A  L  A  A  L  R  A  G  A  V  C  L  P  V  A  P  G

66121  GGCTGCCCCGGCCCGCCCGCTGGCAGCACGCCACCCGGGCCGGGGCGACGGCCGTCCTCA  66180
        L  P  R  P  A  R  W  Q  H  A  T  R  A  G  A  T  A  V  L  T

66181  CCCAGTCCTGGCTCACCCAGCGCATCGACTGGCCGCAGGAACTGCCCGTCCTCTCCGTGG  66240
        Q  S  W  L  T  Q  R  I  D  W  P  Q  E  L  P  V  L  S  V  D

66241  ACGAACCCGGGCCGCCGGTACCACCCACCACCGCCCCGGCCGACGGACGGTCCGCGACCG  66300
        E  P  G  P  P  V  P  P  T  T  A  P  A  D  G  R  S  A  T  D

66301  ACGCCGCCTACCGGCTGGACGCCCCCGTCAGCCACCGCGCGATCACCACCGCCGCCCTGG  66360
        A  A  Y  R  L  D  A  P  V  S  H  R  A  I  T  T  A  A  L  E

66361  AGATCGACCGCGCCTTCCGCGTCGGACCCGGCGACCGGCTCCTGGCCCTGGCCCCCGCCG  66420
        I  D  R  A  F  R  V  G  P  G  D  R  L  L  A  L  A  P  A  D

66421  ACTCGCCGCTCGCTCTCTACGAACTGTTCGGGCCCCTCCTGGCCGGTGCGGCCCTCGTCC  66480
        S  P  L  A  L  Y  E  L  F  G  P  L  L  A  G  A  A  L  V  L

66481  TCACCCGGGACATCGACCTGCGCGATCCCGGAGCCCTGCACGAGGCGCTGCGCACCCACG  66540
        T  R  D  I  D  L  R  D  P  G  A  L  H  E  A  L  R  T  H  G

66541  GCGTCACCCTCTGGCACTCGCCGCCCGCCCTCCTCGGCCTCCTCCTCGACCACCTCGCCG  66600
        V  T  L  W  H  S  P  P  A  L  L  G  L  L  L  D  H  L  A  D

66601  ACCGGGGCGGCAAACTGCCCGAGTCGCTCCGGCTGGTGCTGCTCGGCGGCGAACGCCTCG  66660
        R  G  G  K  L  P  E  S  L  R  L  V  L  L  G  G  E  R  L  D

66661  ACCCCGCCCTCGTCCGCCGCGTCCGCGAGAGCGCCCCGCACCAGCCGGCCGTCGCCCACC  66720
        P  A  L  V  R  R  V  R  E  S  A  P  H  Q  P  A  V  A  H  L

66721  TCTCCTCGGCCACCCCGTCCGGCCCCTGGACCACCTGCCTGGAGACCGGCGACCTCGCCC  66780
        S  S  A  T  P  S  G  P  W  T  T  C  L  E  T  G  D  L  A  P

66781  CGGAATGGCGCTCGGTCCCCGTCGGCGCGCCCCTGCCCAACCAGCGGGCGCACATCCTGT  66840
        E  W  R  S  V  P  V  G  A  P  L  P  N  Q  R  A  H  I  L  S

66841  CCGAGACCCTGCGGCCCTGCCCGGTCTGGGTCACCGGCCGCCTCCACTACGGCGGCGTCG  66900
        E  T  L  R  P  C  P  V  W  V  T  G  R  L  H  Y  G  G  V  A

66901  CCGCCGAGCCCCCCACCGGAGAGGAGCACGCACCCGCGACCGTCCCGCACCCGGAGACCG  66960
        A  E  P  P  T  G  E  E  H  A  P  A  T  V  P  H  P  E  T  G

66961  GCGAACCGCTGCTGCGCACCGGGCTGTTCGCCCGCCTGCTGCCCGAGGGCCTGATCGACG  67020
        E  P  L  L  R  T  G  L  F  A  R  L  L  P  E  G  L  I  D  V

67021  TCGTCGGCGACGAGACCGCCCGGATCAGCGTCCGCGACCGGCCCCTGAACCTCCAGGACA  67080
        V  G  D  E  T  A  R  I  S  V  R  D  R  P  L  N  L  Q  D  T

67081  CCGAGACCGCCCTCGCCGCCCACGAGGACGTGCACTCCGCCGTGGTCGTCCCCGTCGGGC  67140
        E  T  A  L  A  A  H  E  D  V  H  S  A  V  V  V  P  V  G  R

67141  GGGGAGACGAGTCGCTCGCGCGGGTACGGCTCCACCCCGGCGCCACGGCCGGCCCCGACG  67200
        G  D  E  S  L  A  R  V  R  L  H  P  G  A  T  A  G  P  D  E

67201  AACTCCTCGCCCATCTGCGCCGCAAGGTCTCCCCTTACCTGCTGCCCGGCCACATCGAGG  67260
        L  L  A  H  L  R  R  K  V  S  P  Y  L  L  P  G  H  I  E  V

67261  TGGGCGGTCCGCTGCCGCTCACCCGGGACGGGCGCGTGGACCGCGCGCGCGTCACCGCCG  67320
        G  G  P  L  P  L  T  R  D  G  R  V  D  R  A  R  V  T  A  E

67321  AGGCCCCCGCCCCCGCTGCCGTGCCCGCCGCCGCGCCGGCGGCGTCGGCACCCGCGCGGG  67380
        A  P  A  P  A  A  V  P  A  A  A  P  A  A  S  A  P  A  R  D

67381  ACGAGGCCGAACTCCTCGCCCAAGTGGCCCGGGTGACCTGCCGGGTGCTGGGAATCGGCG  67440
        E  A  E  L  L  A  Q  V  A  R  V  T  C  R  V  L  G  I  G  A
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67441  CCGTCGAACCCGATATGAACCTGCTCGACGCCGGTGCCACCTCCGTCGAACTCGTCCGCC   67500
        V  E  P  D  M  N  L  L  D  A  G  A  T  S  V  E  L  V  R  L

67501  TGGCGACCGCTCTGGAGGAGGAACTCGGCCTCGACACCGACATCGAGGAACTGCTGGCCT   67560
        A  T  A  L  E  E  E  L  G  L  D  T  D  I  E  E  L  L  A  F

67561  TCCCGTCGGTCGCCGTGATCGTCGGCCGCCACCTCGGCCGCCGGACGGCACCACCGGCCC   67620
        P  S  V  A  V  I  V  G  R  H  L  G  R  R  T  A  P  P  A  R

67621  GGGACCCCCTGCCGCCCGCGTCCGTAGCGTTCGCACCCGGGTCCGTACTGCCCGCGCCGC   67680
        D  P  L  P  P  A  S  V  A  F  A  P  G  S  V  L  P  A  P  P

67681  CCGCGCCCGGACCCGTGCCGCCCGCGTCCGTGCCGCCCGCACCCGCGTCCGTACCGCCCG   67740
        A  P  G  P  V  P  P  A  S  V  P  P  A  P  A  S  V  P  P  A

67741  CGTCCGAGTCCTCACCGCTCGCGCCGCCCGCACCCGGGCCCGTGCCACCCACGCCCGTCC   67800
        S  E  S  S  P  L  A  P  P  A  P  G  P  V  P  P  T  P  V  P

67801  CGCCCGCCTCCGTCCCGCCCGCGTCCGGGGCCGCGCCGCACGTACCGCCCGCGCCGCCCG   67860
        P  A  S  V  P  P  A  S  G  A  A  P  H  V  P  P  A  P  P  A

67861  CACCCATCCCCGCGCCCTCCGTGCCccccgcgccccgcccccaaccgcccctgctcaccg   67920
        P  I  P  A  P  S  V  P  P  A  P  R  P  Q  P  P  L  L  T  G

67921  gcatcggcgcccgccaggcgTTCAAGGACGCCCACCACGGCATCCGGCACGAGTTCGACG   67980
        I  G  A  R  Q  A  F  K  D  A  H  H  G  I  R  H  E  F  D  A

67981  CCACCGACGGCGTCGCCCTCAGCGGCCCGGACGACCACCACCTCACCGCCCGTCGCAGCC   68040
        T  D  G  V  A  L  S  G  P  D  D  H  H  L  T  A  R  R  S  H

68041  ACCACCGCTTCGACCCCGGCCCCGTGACGCTGCCGGACCTGGCCGCCCTCCTCGGGGCCC   68100
        H  R  F  D  P  G  P  V  T  L  P  D  L  A  A  L  L  G  A  L

68101  TCCGCCGGGTCCGCGGCCCGGGAGGCGAACCCAAATACGCCTATCCGTCGGCCGGTTCCT   68160
        R  R  V  R  G  P  G  G  E  P  K  Y  A  Y  P  S  A  G  S  S

68161  CCTACCCCGTCCAGACCTACCTGCTCGTCCACCCGGGGAAGGTGACCGGACTGCCCGGCG   68220
        Y  P  V  Q  T  Y  L  L  V  H  P  G  K  V  T  G  L  P  G  G

68221  GCAGCCACTACGTCCACCCCGCGCGCAACCGCCTGGTGAGCATCGACCCCACCGCGACCC   68280
        S  H  Y  V  H  P  A  R  N  R  L  V  S  I  D  P  T  A  T  L

68281  TGCCCGCCGACGCGCACGCCGAGATCAACCGCGCCGCCTACGGGGAGGCGGCCTTCTCCC   68340
        P  A  D  A  H  A  E  I  N  R  A  A  Y  G  E  A  A  F  S  L

68341  TCTACCTCATCGCCGCGATCGACGCGATCACACCGCTCTACGGCGATCTCTCCTGGGACT   68400
        Y  L  I  A  A  I  D  A  I  T  P  L  Y  G  D  L  S  W  D  F

68401  TCACCGTCTTCGAGGCCGGTGCCATGACCCAGTTGCTGATGCGGACCGCCGTCGGCACCG   68460
        T  V  F  E  A  G  A  M  T  Q  L  L  M  R  T  A  V  G  T  G

68461  GCATCGGCCTGTGCCCCGTCGGCACGATGGACCCCGCGCCGCTGCGCCGCGCGTTCGCCC   68520
        I  G  L  C  P  V  G  T  M  D  P  A  P  L  R  R  A  F  A  L

68521  TCACCGACCGGCACCGCTTCGTCCACGCCCTCCTCGGCGGGCGGCCCCGCACGGAGGCCC   68580
        T  D  R  H  R  F  V  H  A  L  L  G  G  R  P  R  T  E  A  P

68581  CGTGAACCGGCACGGCCCCCTGGCGGGCCGGCGGCAGAGCGTCGACACCCGCAGCGCCGC   68640
       M  N  R  H  G  P  L  A  G  R  R  Q  S  V  D  T  R  S  A  A   (orf15)
        *

68641  GTGGGTGGCGCCGACGGGCACCCCGGGGCTGCCGCTGGAGGTGGCCGCCACCCGGGACGG   68700
       W  V  A  P  T  G  T  P  G  L  P  L  E  V  A  A  T  R  D  G

68701  CGTCGACCCGGCCGAATGGGCCCGCACCCACCTCGACACCGTCACCGGCTGGCTGCACCG   68760
       V  D  P  A  E  W  A  R  T  H  L  D  T  V  T  G  W  L  H  R

68761  TCACGGAGCCGTCCTGTTCCGCGGCTTCGGCGTCGGCCTCGACGGCTTCGGCGACGTCGT   68820
       H  G  A  V  L  F  R  G  F  G  V  G  L  D  G  F  G  D  V  V

68821  CCACGCCCTGGCCGGATCCCCCGAGGCGTACGTCGAACGGTCGTCGCCGCGCACCGCCCT   68880
       H  A  L  A  G  S  P  E  A  Y  V  E  R  S  S  P  R  T  A  L
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68881  CGGGCATCACCTCTACACCGCCACCGACCACCCCGCCGACCAGCCCATCCCCCCGCACAA  68940
         G  H  H  L  Y  T  A  T  D  H  P  A  D  Q  P  I  P  P  H  N
68941  CGAGAACTCCTACCAACTCCGCTTCCCCGGACGGCTGGTCTTCGGCTGCCTCACCCCGGC  69000
         E  N  S  Y  Q  L  R  F  P  G  R  L  V  F  G  C  L  T  P  A
69001  CCGGACCGGCGGCGCGACCCCGCTCGCCGACACCCGGCGCGTCCTGGGCCGCCTCGACCC  69060
         R  T  G  G  A  T  P  L  A  D  T  R  R  V  L  G  R  L  D  P
69061  CGCCCTCGTCGCCGCCTTCGCCCGCCGCGGGGTGCTCTACCAGCGCAACTACGGCGACGG  69120
         A  L  V  A  A  F  A  R  R  G  V  L  Y  Q  R  N  Y  G  D  G
69121  GATCGGCATGTCCTGGCAGGACGCCTTCCAGACCCGCGACAAGGCGGCCGTCACCGCCTA  69180
         I  G  M  S  W  Q  D  A  F  Q  T  R  D  K  A  A  V  T  A  Y
69181  CTGCGCCGCCCGCCGCGTCGACGTCGAATGGAAACCCGACGGCGGGCTGCGGACCACCCA  69240
         C  A  A  R  R  V  D  V  E  W  K  P  D  G  G  L  R  T  T  Q
69241  GGTCCGCCCCGCCCTCGCCGTCCACCCGGCGACGGGGGAGCGGGTGTGGTTCAACCACGC  69300
         V  R  P  A  L  A  V  H  P  A  T  G  E  R  V  W  F  N  H  A
69301  CGCGTTCTTCCACGTCTCCGCCCGGCCGCCCGCGCTGCGGGACGCCCTGCTGGCCCAGTT  69360
         A  F  F  H  V  S  A  R  P  P  A  L  R  D  A  L  L  A  Q  F
69361  CGACGAACGCGACCTGCCGAGCCACTCCTGCTACGGCGACGGCCGGCCCATCGAACCCGC  69420
         D  E  R  D  L  P  S  H  S  C  Y  G  D  G  R  P  I  E  P  A
69421  CGTCATGGAGGAACTGCACCACGCCTACGCCGCCGAACTGGTGGCGCCCGCCTGGCGGGC  69480
         V  M  E  E  L  H  H  A  Y  A  A  E  L  V  A  P  A  W  R  A
69481  CGGCGACGTCCTCCTCGTCGACAACCTCCTCACCGCGCACGGCAGGGAACCCTTCACCGG  69540
         G  D  V  L  L  V  D  N  L  L  T  A  H  G  R  E  P  F  T  G
69541  CGAACGCCGCGTCGTCGTCGGCATGGCACAGCCGCTGGACTGGGACGAGGTGAGCGCGTG  69600
         E  R  R  V  V  V  V  G  M  A  Q  P  L  D  W  D  E  V  S  A  *
                                                                  M     (orf14)
69601  ACCGCCCCCGGCACACCGCTGCCCGCGACCTTCGTCCAGCGCGGCCTGTGGCCGTCCACT  69660
         T  A  P  G  T  P  L  P  A  T  F  V  Q  R  G  L  W  P  S  T
69661  CGCCACGCCCGCCCGGCGGAGGTCACCCACGTCCGCGCCCTGCGCCTGACCGGGGACACC  69720
         R  H  A  R  P  A  E  V  T  H  V  R  A  L  R  L  T  G  D  T
69721  GACACGGCGCGGCTCACCGAGGCCGTCCGGCGGGTCACCGCCGCCCTCCCCGCCCTCACC  69780
         D  T  A  R  L  T  E  A  V  R  R  V  T  A  A  L  P  A  L  T
69781  GCCGAACTCTCCGGCGACGAGGAACCCCGCCTGACCCTCCGGCCGGACGCCCCCGAGGTC  69840
         A  E  L  S  G  D  E  E  P  R  L  T  L  R  P  D  A  P  E  V
69841  ACCCCGGTCGACCTGCGCGGAGCCCCGTCCGCCGGACGCGACGCCGTCTGCGTGGCGCTG  69900
         T  P  V  D  L  R  G  A  P  S  A  G  R  D  A  V  C  V  A  L
69901  CTGCGCGCCGACCGGGACCACCCTCGCGCCGGACGCCACCGGGCCCGCTTCCACCTGGTG  69960
         L  R  A  D  R  D  H  P  R  A  G  R  H  R  A  R  F  H  L  V
69961  CGGCTCCACGACGACGAGACGGTGCTCGCGCTCACGGCCCACACCCTCCTCCTCGACACA  70020
         R  L  H  D  D  E  T  V  L  A  L  T  A  H  T  L  L  L  D  T
70021  CCGTCTCTCTACGCCGTGCTCGGCGCGGTCTGCCAGGCGTACGCCGGCCGCTTCCGCCCC  70080
         P  S  L  Y  A  V  L  G  A  V  C  Q  A  Y  A  G  R  F  R  P
70081  GAGCACTACCGCGACGCCACCACCCTGCCCGACGCGCCCCACGCCCCCCTCTCCGGTCGG  70140
         E  H  Y  R  D  A  T  T  L  P  D  A  P  H  A  P  L  S  G  R
70141  GCCCGGGCCTCCCGCCGGCGCTGGTGGCACCGGCGCCTGGCCGCCCTGCCCGGCCCGGCC  70200
         A  R  A  S  R  R  R  W  W  H  R  R  L  A  A  L  P  G  P  A
70201  CCGGCCCCCGCCGGCCCGCCCCGCGACCGGGTGACCGAAACCCACCGGCTGCGCATCCCC  70260
         P  A  P  A  G  P  P  R  D  R  V  T  E  T  H  R  L  R  I  P
70261  GCAGCGCGCTGGAAAGCCCTGACCGCCCTGACCGCCCTGGGCGGCCCCCTCGGCGGCAAC  70320
         A  A  R  W  K  A  L  T  A  L  T  A  L  G  G  P  L  G  G  N
70321  GGCTCGCTCGCCGTCATGGCCCTGGCCGCCTGGTGCCTGCGCGCCCCGGACCACCGGGGA  70380
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        G  S  L  A  V  M  A  L  A  A  W  C  L  R  A  P  D  H  R  G
                .     .     .     .     .     .     .     .     .
70381   CCGGCCCGCTTCACCACCGTCGTCGACCTGCGCGACCACCTCGGACTCGGGCCCGCCGTC   70440
        P  A  R  F  T  T  V  V  D  L  R  D  H  L  G  L  G  P  A  V
                .     .     .     .     .     .     .     .     .
70441   GGCCCGTTCACCGACCGCCTCGTCTTCGGCGCCGACCTCGGCGAAGCGCCGCGCCCCTCC   70500
        G  P  F  T  D  R  L  V  F  G  A  D  L  G  E  A  P  R  P  S
                .     .     .     .     .     .     .     .     .
70501   TTCCGGGACGTCACGCTGCGCGCCCAGTCCGGGTTCCTGGACGCCGTCGTGCACTACCTC   70560
        F  R  D  V  T  L  R  A  Q  S  G  F  L  D  A  V  V  H  Y  L
                .     .     .     .     .     .     .     .     .
70561   CCCTACGGCGACGTCGTGGAACTCgGCAGGGAACTGGGCCGCGTCACCGCGCCCCGCACC   70620
        P  Y  G  D  V  V  E  L  G  R  E  L  G  R  V  T  A  P  R  T
                .     .     .     .     .     .     .     .     .
70621   GCCGCGCACTGGGACGTGGCGCTGAACTTCTGCCGCAACCCGCCCACCAGCGCCGCCACC   70680
        A  A  H  W  D  V  A  L  N  F  C  R  N  P  P  T  S  A  A  T
                .     .     .     .     .     .     .     .     .
70681   CGCGGCGAACGCACCCTCGCCGAACGCGGCCTGTCCATCGAGCTGTTCCGCGAGGCCGAC   70740
        R  G  E  R  T  L  A  E  R  G  L  S  I  E  L  F  R  E  A  D
                .     .     .     .     .     .     .     .     .
70741   CTGCTCGGCGCGGCCGGCACCGGTCCCGCGCACCGGTGGGACGGCACGGTGCTCGCCCTC   70800
        L  L  G  A  A  G  T  G  P  A  H  R  W  D  G  T  V  L  A  L
                .     .     .     .     .     .     .     .     .
70801   TCCCTAGGCGAACTCGGCGACGACACCGTGCTGGTCCTCGACGCCGACCGCGACCACCCG   70860
        S  L  G  E  L  G  D  D  T  V  L  V  L  D  A  D  R  D  H  P
                .     .     .     .     .     .     .     .     .
70861   CACCACGGAACCGCCGACCGGCTGCTCCACCGGATGGACGAAGCGCTCCTGGCGGCCGTC   70920
        H  H  G  T  A  D  R  L  L  H  R  M  D  E  A  L  L  A  A  V
                .     .     .     .     .     .     .     .     .
70921   GCCGACCCGGACGCCCCCCTGCCCCCCTTGCCCGCCCCCGCGCACACCACGAGGAGCCAC   70980
        A  D  P  D  A  P  L  P  P  L  P  A  P  A  H  T  T  R  S  H
                .     .     .     .     .     .     .     .     .
70981   CGATGACCACGACCCCGCGGACCGCCGCCGAGCCCACCTACCACGTGGTGGTCAACGACG   71040
          M  T  T  T  P  R  T  A  A  E  P  T  Y  H  V  V  V  N  D  E   (orf13)
        R  *
                .     .     .     .     .     .     .     .     .
71041   AGGAGCAGTACTCGATCTGGCTCGCCGAACAGGAGATCCCGGCCGGCTGGCGGGCCACCG   71100
          E  Q  Y  S  I  W  L  A  E  Q  E  I  P  A  G  W  R  A  T  G
                .     .     .     .     .     .     .     .     .
71101   GAACCTCCGGCACCCAGGAGGAGTGCCTGCGCCACATCGACGAGGTGTGGACCGACATGC   71160
          T  S  G  T  Q  E  E  C  L  R  H  I  D  E  V  W  T  D  M  R
                .     .     .     .     .     .     .     .     .
71161   GCCCCCGCAGCCTGCGCGAGGCCATGGCCGCGGCGGAGCACGCGGAGCCCGCTCCCGCCC   71220
          P  R  S  L  R  E  A  M  A  A  A  E  H  A  E  P  A  P  A  P
                .     .     .     .     .     .     .     .     .
71221   CGGCCCCGGCCGAGGAGGAGCCGAGCCTCGTCGACCGGCTCTGCGCGGGCGACCAGCCGG   71280
          A  P  A  E  E  E  P  S  L  V  D  R  L  C  A  G  D  Q  P  V
                .     .     .     .     .     .     .     .     .
71281   TGGAGTCGGTCCTCCGCCCGGAGCGCACGGCCGCCGCCCTGCGGGAGGCCGTCGACCGCG   71340
          E  S  V  L  R  P  E  R  T  A  A  A  L  R  E  A  V  D  R  G
                .     .     .     .     .     .     .     .     .
71341   GCTACGTCTTCGTCCGCTTCGCCGCCACCCGCGGCGGCACCGAACTCGGCGTCGCCGTCG   71400
          Y  V  F  V  R  F  A  A  T  R  G  G  T  E  L  G  V  A  V  D
                .     .     .     .     .     .     .     .     .
71401   ACCCCGCGGCGACCACCATGGACGGCACCGAGCTGCGCCTGACCGGCACCCTCACCCTCG   71460
          P  A  A  T  T  M  D  G  T  E  L  R  L  T  G  T  L  T  L  D
                .     .     .     .     .     .     .     .     .
71461   ACTTCGAACCGGTCCGCTGCCACGCCCGCGTCGACGTGACCACCTTCACGGGCGAGGGCC   71520
          F  E  P  V  R  C  H  A  R  V  D  V  T  T  F  T  G  E  G  R
                .     .     .     .     .     .     .     .     .
71521   GCCTGGAGCGCGTGTCCGGCACCTGACCCCCGCCGGCCACCCGGCCGTGAGGCGCGGCTC   71580
          L  E  R  V  S  G  T  *
                .     .     .     .     .     .     .     .     .
71581   GGGACCGGGCCGCCGACCCACCGAAGGGAGGGACCCCATGACCACCCCCATGACCACCCC   71640
                                          M  T  T  P  M  T  T  P   (orf12)
                .     .     .     .     .     .     .     .     .
71641   CACGACCACCCGCACCACCACCCGCACCGCCGTCTTCGCCCACCTCCGCGCCCCCGGCCT   71700
          T  T  T  R  T  T  T  T  R  T  A  V  F  A  H  L  R  A  P  G  L
                .     .     .     .     .     .     .     .     .
71701   CGGCGACCTCCTCCAGCGCAACATCGGCCTCGCCCTCGTCCGCCGCGCCCGCCCGGCGAC   71760
          G  D  L  L  Q  R  N  I  G  L  A  L  V  R  R  A  R  P  A  T
                .     .     .     .     .     .     .     .     .
71761   GGCGGTCACCCTGGTCGTCGGCGAGGACCTGGCGGCCCGCTTCGGTCCGGCACTCACCCG   71820
          A  V  T  L  V  V  G  E  D  L  A  A  R  F  G  P  A  L  T  R
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71821  CCACACGTACGCCACCGACGTGCTGCCCTGCCCCCAGCGGGGCGAGGCCGACCCCCGGTG   71880
         H  T  Y  A  T  D  V  L  P  C  P  Q  R  G  E  A  D  P  R  W

71881  GCCCGCCTTCCTGCGCACCCTGGCCGACCGCCGCTTCGCCCTCGCCGTCGTCGACCCGGA   71940
         P  A  F  L  R  T  L  A  D  R  R  F  A  L  A  V  V  D  P  D

71941  CAGCCAGGGCCTGCACGCCGGCCACGCCCGGGCCGCCGGCGTGCCCGAGCGGATCGGCCT   72000
         S  Q  G  L  H  A  G  H  A  R  A  A  G  V  P  E  R  I  G  L

72001  GCCGCAGGACCGGCCCGGAGACGAACACATCACCCATCCCATCCGCCTCCCACGTCCCCT   72060
         P  Q  D  R  P  G  D  E  H  I  T  H  P  I  R  L  P  R  P  L

72061  GTGGGGGACCCCGGACCTGTACGAGTACGCCACTGCCCTCGCCGCCGCGCTGGGCCTGCC   72120
         W  G  T  P  D  L  Y  E  Y  A  T  A  L  A  A  A  L  G  L  P

72121  CGCACCGCCGCGCCCCGGCGACGTCCTGCCGGAGCTGCCCCGCACCCGCGGCGTCCGCCC   72180
         A  P  P  R  P  G  D  V  L  P  E  L  P  R  T  R  G  V  R  P

72181  GCCGACGGCCGGTCTGCCCCGTCCGCTCGTCGCCGTCCACCCCGGCGGGGCACCGCACTG   72240
         P  T  A  G  L  P  R  P  L  V  A  V  H  P  G  G  A  P  H  W

72241  GAACAGGAGATGGCCGCTCGAGCACTACGCCCGGCTCTGCGCCCGCCTCGCGGCCGAACT   72300
         N  R  R  W  P  L  E  H  Y  A  R  L  C  A  R  L  A  A  E  L

72301  CTCGGCCTCCCTCTGCCTGCTGGGCGACGAAGCCGAACGCCCCGAGCTGGAACTGCTCCG   72360
         S  A  S  L  C  L  L  G  D  E  A  E  R  P  E  L  E  L  L  R

72361  GCACGCCGTCCTGACGCGGTCCCCGCGAGCCGTCGTCCACCTCGAGGCGGGCGCGGACCT   72420
         H  A  V  L  T  R  S  P  R  A  V  V  H  L  E  A  G  A  D  L

72421  CGACCGGACCGCGAACGTCCTCGCCGACGCCGACCTGCTCGTCGGCAACGACTCCTCGCT   72480
         D  R  T  A  N  V  L  A  D  A  D  L  L  V  G  N  D  S  S  L

72481  CGCCCACGTCGCCGCCGCCGTCCGCACCCCGTCCGTCGTCCTCTACGGCCCGACCGGCAC   72540
         A  H  V  A  A  A  V  R  T  P  S  V  V  L  Y  G  P  T  G  T

72541  CGAGTACCTGTGGACCAGGATCTACCCGTACCACCGCGGGGTCTCCCTGCGGTGGCCGTG   72600
         E  Y  L  W  T  R  I  Y  P  Y  H  R  G  V  S  L  R  W  P  C

72601  CCAGCGGCTGCGGCACGCCGCAGGCGAACTCGCCGGCCGGCGGTGCGCGCACGGCTGCGT   72660
         Q  R  L  R  H  A  A  G  E  L  A  G  R  R  C  A  H  G  C  V

72661  CCTGCCCTACCAGGGCCCGGCCGGCCCGTATCCGCGCTGTCTGGCCGACCTGCCGGTGGA   72720
         L  P  Y  Q  G  P  A  G  P  Y  P  R  C  L  A  D  L  P  V  D

72721  CAGGGTCTGGCCGGCGGTGACCGCCCGATGGGCGAGCCCCCACCCCGTGACGATCAGGAG   72780
         R  V  W  P  A  V  T  A  R  W  A  S  P  H  P  V  T  I  R  S

72781  TACCCCATGAGCGCCGACCCGTCCCGGGTGCGGACGATCCTCTCCGTCAACTTCAACCAC   72840
         T  P  *
               M  S  A  D  P  S  R  V  R  T  I  L  S  V  N  F  N  H    (orf11)

72841  GACGGCTCCGGCGTGCTGTTGCGGGAGGGCAGGATCGCCGGCTACGTCACCACCGAGCGC   72900
         D  G  S  G  V  L  L  R  E  G  R  I  A  G  Y  V  T  T  E  R

72901  CGCTCCCGCCTCAAGAAGCACCCGGGCCTGCGCGAGGAGGACCTCGACGAACTGCTGGAC   72960
         R  S  R  L  K  K  H  P  G  L  R  E  E  D  L  D  E  L  L  D

72961  CAGGCCGGGGCCGACCTCTCCGACATCGACCACGTCATGCTCTGCAACCTGCACACCATG   73020
         Q  A  G  A  D  L  S  D  I  D  H  V  M  L  C  N  L  H  T  M

73021  GACACACCCGACATACCCCGGCTGCACGGCTCCGACCTCAAGGAGACCTGGCTCGCGTTC   73080
         D  T  P  D  I  P  R  L  H  G  S  D  L  K  E  T  W  L  A  F

73081  TGGGTCAACCAGCGCAACGACGAGGTGAGCCTGCGCGGCCGCCGCATCCCCTGCACCGTC   73140
         W  V  N  Q  R  N  D  E  V  S  L  R  G  R  R  I  P  C  T  V

73141  AACCCGGACCACCACCTCATCCACGCCGCCACCGCCTACTACACCTCCGGCTACGACTCG   73200
         N  P  D  H  H  L  I  H  A  A  T  A  Y  Y  T  S  G  Y  D  S

73201  GCGATGGCCGTGGCCATCGACCCCACCGGCTGCCGCGCCTTCGCCGGCAAGGGCAGCCGC   73260
         A  M  A  V  A  I  D  P  T  G  C  R  A  F  A  G  K  G  S  R
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73261  CTCTACCCCCTGCGCCGCGACCTCGACGCCTGGTTCAACGCCAACATCGGCTACTGCTAC  73320
       L  Y  P  L  R  R  D  L  D  A  W  F  N  A  N  I  G  Y  C  Y

73321  GTCGCCGACCTGATGTTCGGCTCCAGCATCGTCGGCGCCGGCAAGGTCATGGGCCTCGCC  73380
       V  A  D  L  M  F  G  S  S  I  V  G  A  G  K  V  M  G  L  A

73381  CCCTACGGCAGACCCGCCGACGGCGCCGGCCCCGACGAGGAACCGCCCGAGACCGTGCGC  73440
       P  Y  G  R  P  A  D  G  A  G  P  D  E  E  P  P  E  T  V  R

73441  GACTTCGCCGCCCTGGTGGCCCTGGCCGACCGGCACCCGCGCCTCGTCGACGTCGACGGC  73500
       D  F  A  A  L  V  A  L  A  D  R  H  P  R  L  V  D  V  D  G

73501  AGGAAGCTCAACGCCACCCTCGCCCACTACATCCAGCTGGGCCTGGAACGCCAGCTGACC  73560
       R  K  L  N  A  T  L  A  H  Y  I  Q  L  G  L  E  R  Q  L  T

73561  GCCGTCTTCGCCGAGCTCGCCCCGCTGTGCGCCCGCAACGGCATCGCACCGGACATCTGC  73620
       A  V  F  A  E  L  A  P  L  C  A  R  N  G  I  A  P  D  I  C

73621  CTCTCCGGCGGTACCGCCCTCAACGCCATCGCCACCCAACTCGCCTTCGAGTCGACCGGC  73680
       L  S  G  G  T  A  L  N  A  I  A  T  Q  L  A  F  E  S  T  G

73681  TTCGAGCGCATGCACCTCCACCCCGCCTGCGGCGACGACGGCACCGCGATCGGCGCGGCG  73740
       F  E  R  M  H  L  H  P  A  C  G  D  D  G  T  A  I  G  A  A

73741  CTCTGGCACTGGCACCACGTCCTGGGCCACCCCCGGCTCCACCACACCAACGCCGACCTC  73800
       L  W  H  W  H  H  V  L  G  H  P  R  L  H  H  T  N  A  D  L

73801  ATGTACTCCGTCCGTGAGTACCCCGAGCACACCGTCCGGCGGGCCGTGCGGGACCACGCG  73860
       M  Y  S  V  R  E  Y  P  E  H  T  V  R  R  A  V  R  D  H  A

73861  GCCGACCTCGTCGTCGAGGAGACCGGCGACTACGTCGCCAGGGCCGCCGAACTGGTCGCC  73920
       A  D  L  V  V  E  E  T  G  D  Y  V  A  R  A  A  E  L  V  A

73921  GGCGGCGCCGTCATCGGCTGGTACGACGGCGCCGGCGAGGTCGGGCCGCGGGCCCTGGGC  73980
       G  G  A  V  I  G  W  Y  D  G  A  G  E  V  G  P  R  A  L  G

73981  CACCGCAGCATCGTCGCCGACCCGCGCGACCCCGCCATGCGGGACCGGCTCAACTCCCAG  74040
       H  R  S  I  V  A  D  P  R  D  P  A  M  R  D  R  L  N  S  Q

74041  GTCAAGTTCCGCGAACACTTCCGGCCcTTCGCGCCGTCCGTGCTCAAGGAGCACGCCGCG  74100
       V  K  F  R  E  H  F  R  P  F  A  P  S  V  L  K  E  H  A  A

74101  GAGTGGTTCGGCCTCTCCGACAGCCCCTTCATGCTGCGGGCCACCCCCGTCCTCAAGCCC  74160
       E  W  F  G  L  S  D  S  P  F  M  L  R  A  T  P  V  L  K  P

74161  GGCGTGCCCGCCATCACCCACGTCGACGGGACGTCGAGGATCCAGTCGGTCACCCGCCAG  74220
       G  V  P  A  I  T  H  V  D  G  T  S  R  I  Q  S  V  T  R  Q

74221  GACACCCCCGCCTTCCACGACCTCATCCACGCCTTCAAGGACCGTACGGGGATCCCCATG  74280
       D  T  P  A  F  H  D  L  I  H  A  F  K  D  R  T  G  I  P  M

74281  GTGCTCAACACCAGCCTCAACACCAAGGGCGAGCCGATCGCGGAGACACCCGAGGACGCC  74340
       V  L  N  T  S  L  N  T  K  G  E  P  I  A  E  T  P  E  D  A

74341  CTGCGCACCCTGCTCGGCTCCCGGCTCGACCACCTGGTGCTCCCGGGCCTCATCGTCAGC  74400
       L  R  T  L  L  G  S  R  L  D  H  L  V  L  P  G  L  I  V  S

74401  GGCCGGACGGCGGCCCGCTCATGAGCGCCCCGCGGGGCGAGCGGACCCGGCGCCGCGCGC  74460
                          M  S  A  P  R  G  E  R  T  R  R  R  A  L  (orf10)
       G  R  T  A  A  R  S  *

74461  TCGAACGCGACATCGCCGCGATCTGGGCCGAGACCCTCGGCAGGGACAGCGTCGGCCCGC  74520
         E  R  D  I  A  A  I  W  A  E  T  L  G  R  D  S  V  G  P  H

74521  ACGAGGACTTCGCCGCGCTGGGCGGCAACTCCATCCACGCCATCAAGATCACCAACCGGG  74580
         E  D  F  A  A  L  G  G  N  S  I  H  A  I  K  I  T  N  R  V

74581  TGGAGGAACTCGTCGACGCCGAGCTGTCCATCCGCGTCCTGCTCGAGACGCGCACCGTGG  74640
         E  E  L  V  D  A  E  L  S  I  R  V  L  L  E  T  R  T  V  A

74641  CCGGCATGACGGACCACGTCCACGCCACGCTCACGGGGGAGCGGGACCGGTGAACACCGA  74700
         G  M  T  D  H  V  H  A  T  L  T  G  E  R  D  R  *
                                                    M  N  T  D    (orf9)
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74701  CCTGCCCCGGCTGCTCGACCGGATCGCCGGCCTGCGCGTCCTCGTCATCGGCGACGTCAT  74760
         L  P  R  L  L  D  R  I  A  G  L  R  V  L  V  I  G  D  V  I
74761  CCTCGACACCTACGTCTGGGGAGCCACCTCGGGCCTGTGCCGCGAATCCCCCGTCCCTGC  74820
         L  D  T  Y  V  W  G  A  T  S  G  L  C  R  E  S  P  V  P  A
74821  CGTCACCCTGACCTCCGTCGCCCACCAGTGCGGCGGCGCCGCCAACGTCGCCGTGAACCT  74880
         V  T  L  T  S  V  A  H  Q  C  G  G  A  A  N  V  A  V  N  L
74881  CCGGGCGCTCGGCGCCGAACCGGTGCTGCTCTCCGCGACGGGTGACGACCGCGCCGGCCG  74940
         R  A  L  G  A  E  P  V  L  L  S  A  T  G  D  D  R  A  G  R
74941  CCGGCTGCGCGAAGCCCTCCGTGCGCGGGACGTCGACACCGGCGGACTCTTCGTACAGCC  75000
         R  L  R  E  A  L  R  A  R  D  V  D  T  G  G  L  F  V  Q  P
75001  CGGCCGGACCACGGTCACCAAACGCCGCGTCATGGCCGACGGACAGATGCTGCTCCGCCT  75060
         G  R  T  T  V  T  K  R  R  V  M  A  D  G  Q  M  L  L  R  L
75061  CGACGAGGGCGGCGAACACCCGTTGCCCGTGGCGACGGACACCGGAAGCCGCCTGCTCGA  75120
         D  E  G  G  E  H  P  L  P  V  A  T  D  T  G  S  R  L  L  E
75121  ACGGGCCGCCGGCCTGCTGCCCGCCGTCGACGCCGTGATCGTCTCCGACTACGGGTACGG  75180
         R  A  A  G  L  L  P  A  V  D  A  V  I  V  S  D  Y  G  Y  G
75181  CGTGTGGGAGCCCGACACCGTCGCCCGGCTCGCCGCACACCGCGAACTCGGCCCGTCCAC  75240
         V  W  E  P  D  T  V  A  R  L  A  A  H  R  E  L  G  P  S  T
75241  CCTGGTCGTCGACTCCCGCCGGCCCGCGCGCTTCACCGCGCTGCGGGCCAGCGCCGTCAA  75300
         L  V  V  D  S  R  R  P  A  R  F  T  A  L  R  A  S  A  V  K
75301  ACCCAACCACGCGGAGGCGCTGCGCCTGCTCGACGCCGGCGAACCCCCGCCCGGCCCGGC  75360
         P  N  H  A  E  A  L  R  L  L  D  A  G  E  P  P  P  G  P  A
75361  CAGGGCGGACTGGGCGGCCGCCCTCGGCGACCGGCTCCTGCGCCTGACGGGAGCCGAACG  75420
         R  A  D  W  A  A  A  L  G  D  R  L  L  R  L  T  G  A  E  R
75421  GGTCGCCCTCACCCTGGACGCCGACGGATCACTGCTCTTCGAACGCGACCGGCCCCCGGT  75480
         V  A  L  T  L  D  A  D  G  S  L  L  F  E  R  D  R  P  P  V
75481  CCGCACGTTCGCCCGGGGCAGCCGGGCACCGGTCACGGCCGCCGTCGGCGCCGGCGACGC  75540
         R  T  F  A  R  G  S  R  A  P  V  T  A  A  V  G  A  G  D  A
75541  CTTCACCGCGGCCCTCACCCTCGCCCTCGCCGCCGGCGCCGACTCCGCGGTCGCCGCCGA  75600
         F  T  A  A  L  T  L  A  L  A  A  G  A  D  S  A  V  A  A  E
75601  ACTGGCCTCCGCCGCCGCCGGCACGGCCGTCGCCACCCCCGGCACCAGCACCTGGCACGC  75660
         L  A  S  A  A  A  G  T  A  V  A  T  P  G  T  S  T  W  H  A
75661  CGACGAACTGCGCCGACTGCTCGGCGGCACCGGCAAGGTCTGCCGGACCGGCACCCTGCC  75720
         D  E  L  R  R  L  L  G  G  T  G  K  V  C  R  T  G  T  L  P
75721  CGCCCGGCTGCTCGACCCGGCCGCCCGCGACCGCCGGGTCGTCTTCACCAACGGCTGCTT  75780
         A  R  L  L  D  P  A  A  R  D  R  R  V  V  F  T  N  G  C  F
75781  CGACCTCCTGCACGGCGGCCACGTCTCCTGCCTGAGCCGGGCCAAGGAACTGGGCGACCT  75840
         D  L  L  H  G  G  H  V  S  C  L  S  R  A  K  E  L  G  D  L
75841  GCTCGTCGTCGGCGTCAACTCCGACGCGAGCGTCCGACGCCTCAAGGGCCCCCGTCGCCC  75900
         L  V  V  G  V  N  S  D  A  S  V  R  R  L  K  G  P  R  R  P
75901  GGTGATCCCCCTCGCCGAACGCATGCGCGTCCTCGCCGCCCTGAGCTGCGTGGACCTCGT  75960
         V  I  P  L  A  E  R  M  R  V  L  A  A  L  S  C  V  D  L  V
75961  CGTGCCCTTCGACGACGACAGCCCCGCCGCCCTCATCGAGGCCCTCCGCCCCGAGGTCTA  76020
         V  P  F  D  D  D  S  P  A  A  L  I  E  A  L  R  P  E  V  Y
76021  CGCCAAGGGCGGGGACTACACCCTCGCGACCCTGCCCGAAGCACCCCTCGTCCAACGGCT  76080
         A  K  G  G  D  Y  T  L  A  T  L  P  E  A  P  L  V  Q  R  L
76081  CGGCGGCGTCGTCCACCTGCTCCCCAGCGTCGCCGACACCTCCACCACCGACATCATCCG  76140
         G  G  V  V  H  L  L  P  S  V  A  D  T  S  T  T  D  I  I  R
76141  GCGCATCCACGCCCTGTCCAGGACCGGCGAGGGAGACACCCCATGAGCCACGCCATCGGA  76200
                                                  M  S  H  A  I  G   (orf8)
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          R  I  H  A  L  S  R  T  G  E  G  D  T  P  *
                .     .     .     .     .     .     .
76201  CCGAGCCGGCTGATCCCCGCCATCCGCGAAGCGCTCGGGGACGAGAAGGACCCCCGGCTC  76260
       P  S  R  L  I  P  A  I  R  E  A  L  G  D  E  K  D  P  R  L
                .     .     .     .     .     .     .
76261  GCCCTCTACGTCCACGTCCCCTTCTGCTCCTCCAAGTGCCACTTCTGCGACTGGGTCACC  76320
       A  L  Y  Y  V  H  V  P  F  C  S  S  K  C  H  F  C  D  W  V  T
                .     .     .     .     .     .     .
76321  GACATCCCCGTCGCACGCCTGCGCGGCGACAGCCGGGAACGCTCGCCCTACGTCACCGCC  76380
       D  I  P  V  A  R  L  R  G  D  S  R  E  R  S  P  Y  V  T  A
                .     .     .     .     .     .     .
76381  CTCTGCGACCAGATCCGCTTCTACGGCCCCCAGCTCACCCGGCTCGGCTACCGCCCCGAG  76440
       L  C  D  Q  I  R  F  Y  G  P  Q  L  T  R  L  G  Y  R  P  E
                .     .     .     .     .     .     .
76441  GTCATGTACTGGGGCGGCGGCACCCCCACCCGGCTCACCGGCGACGAGATGACGGCCGTC  76500
       V  M  Y  W  G  G  G  T  P  T  R  L  T  G  D  E  M  T  A  V
                .     .     .     .     .     .     .
76501  CACCAGGCCCTCGACGACGCCTTCGACCTGACGGGACTCCGCCAGTGGTCGGTGGAGAGC  76560
       H  Q  A  L  D  D  A  F  D  L  T  G  L  R  Q  W  S  V  E  S
                .     .     .     .     .     .     .
76561  ACCCCGAACGACCTCGACCCCGCCACCCTCGACACCCTGCGCGGCCTCGGCGTCACCCGC  76620
       T  P  N  D  L  D  P  A  T  L  D  T  L  R  G  L  G  V  T  R
                .     .     .     .     .     .     .
76621  GTCAGCGTCGGCGTCCAGTCGCTCAACCCGTACCAGCTGCGCAAGGCAGGCCGGGCCCAC  76680
       V  S  V  G  V  Q  S  L  N  P  Y  Q  L  R  K  A  G  R  A  H
                .     .     .     .     .     .     .
76681  TCGCGCGAACAGGCCCTGGCCGCCGTCCCCCTGTTGCGCCGCGCCGGCATCGACGAGTTC  76740
       S  R  E  Q  A  L  A  A  V  P  L  L  R  R  A  G  I  D  E  F
                .     .     .     .     .     .     .
76741  AACGTCGACCTGATCGCCGGCTTCCCCGGCGAAGCCGTCGAGTCCTTCGAGGAGACCCTG  76800
       N  V  D  L  I  A  G  F  P  G  E  A  V  E  S  F  E  E  T  L
                .     .     .     .     .     .     .
76801  CGCACCGTCCTCGCGCTCGACCCGCCGCACGTCTCCGTCTACCCCTACCGCGCCACCCCC  76860
       R  T  V  L  A  L  D  P  P  H  V  S  V  Y  P  Y  R  A  T  P
                .     .     .     .     .     .     .
76861  AAGACGGTCATGGCCATGCAGCTCGACCGCGAGTTCGTCGAGGCCCGGAACCGGGACGGC  76920
       K  T  V  M  A  M  Q  L  D  R  E  F  V  E  A  R  N  R  D  G
                .     .     .     .     .     .     .
76921  ATGATCGACGCCTATGAACGGGCCATGGCCGCGCTCGGCGCCGCCGGCTATCACGAGTAC  76980
       M  I  D  A  Y  E  R  A  M  A  A  L  G  A  A  G  Y  H  E  Y
                .     .     .     .     .     .     .
76981  TGCCACGGCTACTGGGTGCGCGACGCGCGCCACGAGGACCAGGACGGCAACTACAAGTAC  77040
       C  H  G  Y  W  V  R  D  A  R  H  E  D  Q  D  G  N  Y  K  Y
                .     .     .     .     .     .     .
77041  GACCTGGCCGGCGACAAGATCGGCTTTGGCAGCGGCGCCGAATCGATCATCGGTCACCAC  77100
       D  L  A  G  D  K  I  G  F  G  S  G  A  E  S  I  I  G  H  H
                .     .     .     .     .     .     .
77101  CTGCTCTGGAACGAGAACAGCGCCTACGCCCGCTACCTGCTCGCCCCCCCGCGAGTTCTCC  77160
       L  L  W  N  E  N  S  A  Y  A  R  Y  L  L  A  P  R  E  F  S
                .     .     .     .     .     .     .
77161  GCCGCCCACCGGTTCACCACCGCCGAACCCGACCGCCTGACCGCCCCCGTCGGCGGCGCG  77220
       A  A  H  R  F  T  T  A  E  P  D  R  L  T  A  P  V  G  G  A
                .     .     .     .     .     .     .
77221  CTGATGACCCGTGAAGGCGTGGTCTTCGCCCGCTTCCGCAGACTGACCGGCCTGGACTTC  77280
       L  M  T  R  E  G  V  V  F  A  R  F  R  R  L  T  G  L  D  F
                .     .     .     .     .     .     .
77281  GCGGACGTCCGCGCCACACCGTACTTCCGCCAGTGGTTCGAGCTCCTGGAGCGCTGCGGC  77340
       A  D  V  R  A  T  P  Y  F  R  Q  W  F  E  L  L  E  R  C  G
                .     .     .     .     .     .     .
77341  GGCCGCTTCGTCGAGACGCCGTACAGCCTCCGCCTGGAGCCGTCCACCATCCACCGCGCC  77400
       G  R  F  V  E  T  P  Y  S  L  R  L  E  P  S  T  I  H  R  A
                .     .     .     .     .     .
77401  TACATCACCCACCTCGCCTACACCATGGCCCATGGCCTGGCCCCCGAACGCGCCTGA      77457
       Y  I  T  H  L  A  Y  T  M  A  H  G  L  A  P  E  R  A  *
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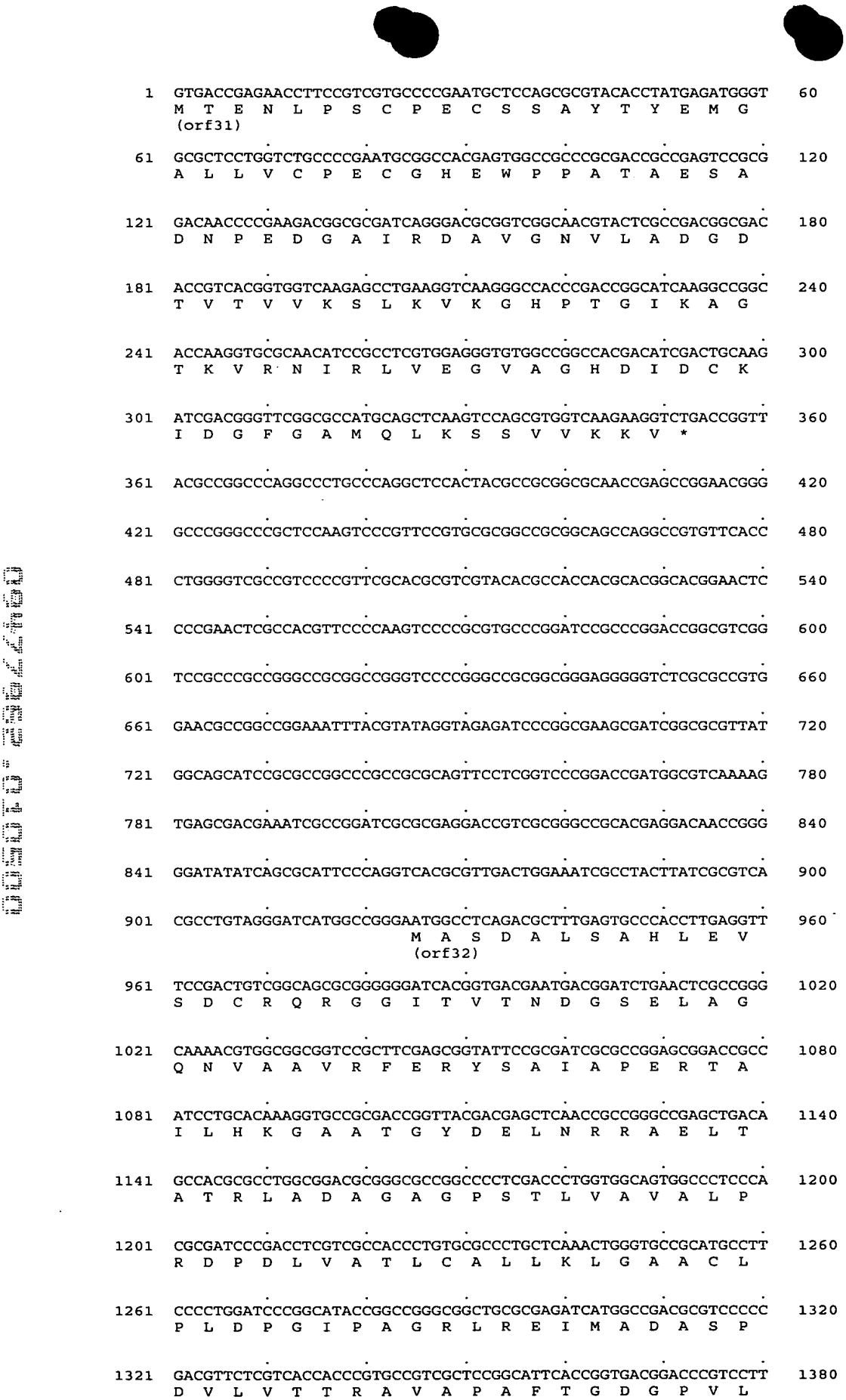
SEQ ID NO: 2 ORFS BLM gene cluster ORFs 31-40
(notice this part is on the reverse strand and the last nucleotide (18660) is the first (1) on the whole cluster of 77457 bp. Also the last orf (40) is incomplete and contains frame shifts)



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1381  TTCCTGGACGACGCTCCTCCGACCTGCTCCGCCGTCCTTCCACGGCACTCAGCGGGGACC  1440
      F  L  D  D  A  P  P  T  C  S  A  V  L  P  R  H  S  A  G  T

1441  GCGTCGGAAATCGCCTATGTGCTGTACCCGACGACTCCTGACGAGAAGTCCGAAAATTCG  1500
      A  S  E  I  A  Y  V  L  Y  P  T  T  P  D  E  K  S  E  N  S

1501  GTCGTCTCCTATCGTGATATGGCGCGCTACCTTGACGACCCCACTGCCGGGATTCCGGCG  1560
      V  V  S  Y  R  D  M  A  R  Y  L  D  D  P  T  A  G  I  P  A

1561  AGGGCGGAGATTCTCCGGCTGGTCGCGCCGCTCCTGTCCGGCGGTCGTCTGGTGCTGGAC  1620
      R  A  E  I  L  R  L  V  A  P  L  L  S  G  G  R  L  V  L  D

1621  GCCGACGAGACCCGGCCCCGGCCGGTCACCCGTGAGGCGCCGCGCGACATGGTGGAGGAC  1680
      A  D  E  T  R  P  R  P  V  T  R  E  A  P  R  D  M  V  E  D

1681  GTCGTGGCGCAGGTCTGGTGCGCCGTGCTCGGCGTGGACCGGGTGGGCGTGCGGGACCGC  1740
      V  V  A  Q  V  W  C  A  V  L  G  V  D  R  V  G  V  R  D  R

1741  TTCTTCGACCTGGGCGGCAAGTCGCTGGCGGCGGTCCAGGTGGTGGCGCGCCTGCGGAAG  1800
      F  F  D  L  G  G  K  S  L  A  A  V  Q  V  V  A  R  L  R  K

1801  CTGCTCGGCGTCGAGCTGCCGCTGCGGGCCCTGTTCGACGCGCCGACGGTCGAGGAGCTG  1860
      L  L  G  V  E  L  P  L  R  A  L  F  D  A  P  T  V  E  E  L

1861  GCCGCCCGGGTGCGGGCCGAACAGGCCGGCGGCCAGGGCGTCCGGGAGGAGGCGGCGCTC  1920
      A  A  R  V  R  A  E  Q  A  G  G  Q  G  V  R  E  E  A  A  L

1921  GAGCCGGTGGGCCGGAGCGAGCCGCTGCCGCTGTCGTTCGCACAGCAACGCCTGTGGTTC  1980
      E  P  V  G  R  S  E  P  L  P  L  S  F  A  Q  Q  R  L  W  F

1981  CTGGACCGCTTGATGCCCGACCGCGCCTTCTACACGATGTGCGACGCGTTCCGCGTCCGG  2040
      L  D  R  L  M  P  D  R  A  F  Y  T  M  C  D  A  F  R  V  R

2041  GGCGGGATCGACCTGGGTGCGCTGCGGCGGGCCCTGCGGATGCTGGTGGGACGGCACGAG  2100
      G  G  I  D  L  G  A  L  R  R  A  L  R  M  L  V  G  R  H  E

2101  ACGCTGCGGACGGCGTTCGTCGAGCGGGACGGTGTGCCGTACCAGCTCGTCGGTCCGGCC  2160
      T  L  R  T  A  F  V  E  R  D  G  V  P  Y  Q  L  V  G  P  A

2161  GACGGGCCCGGTGCGCGGCGCGTGGCCGCTCCCACGCGGGTCGACCTGTCGCTGCTGGAG  2220
      D  G  P  G  A  R  R  V  A  A  P  T  R  V  D  L  S  L  L  E

2221  CCCGCCGAGCGGGAGGAGGCGGTGCGGAACCTGGTGGCGGCGGAGGCGCGGACCCCGTTC  2280
      P  A  E  R  E  E  A  V  R  N  L  V  A  A  E  A  R  T  P  F

2281  CGGCCGGCGGACGGCGCGCTGCTGCGCGTGGTGGTGGCCCGGCTGGCGGACGATGATCAC  2340
      R  P  A  D  G  A  L  L  R  V  V  V  A  R  L  A  D  D  D  H

2341  GTGCTGGTGGTCAGCACGCACCACATCGTCTCCGACGCCTGGTCCGTGGGTGTGCTGGTG  2400
      V  L  V  V  S  T  H  H  I  V  S  D  A  W  S  V  G  V  L  V

2401  GACGAACTCGGACGGCTGTACCGCGAGTGCGTCACCGGAGATCCCGCCGCGCTGCCCCCG  2460
      D  E  L  G  R  L  Y  R  E  C  V  T  G  D  P  A  A  L  P  P

2461  CCGGCCGTCCAGTACGCCGACTTCGCGGTCTGGCAGCGGGCCTGGATGGCCGGTCCGGTG  2520
      P  A  V  Q  Y  A  D  F  A  V  W  Q  R  A  W  M  A  G  P  V

2521  CAGGAGGAGCATCTCGCGTACTGGAAGCGGGCCTTGGACGGCGCTCCCTCGGTGCTGCGG  2580
      Q  E  E  H  L  A  Y  W  K  R  A  L  D  G  A  P  S  V  L  R

2581  CTGCCCATGGACCACCCGCGGCCCGCCGTGCAGTCCGAGCGGGGCGAGACGGTCGGGTTC  2640
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      L  P  M  D  H  P  R  P  A  V  Q  S  E  R  G  E  T  V  G  F

2641  GCGCTGCCCGACGCGCTGGTCGCCGCGCTGGAGAAGCTGGGCCGGGAGCAGGGCGCCACC  2700
      A  L  P  D  A  L  V  A  A  L  E  K  L  G  R  E  Q  G  A  T

2701  CTGTTCATGACGCTGCTCGGCGCCTTCCAGGTCCTGCTGGCGCGTCACGCCGGGCAAGAG  2760
      L  F  M  T  L  L  G  A  F  Q  V  L  L  A  R  H  A  G  Q  E

2761  GACATCGTGGTCGGCGTGCCGGCGGCGGGGCGCACCCGGACCGAGACGGAACCTCTGGTC  2820
      D  I  V  V  G  V  P  A  A  G  R  T  R  T  E  T  E  P  L  V

2821  GGCTTCTTCGTCAACACGCTTCCCTTGCGGGCGATCTGCGCTCCGGGCCTGTCGTTCCGG  2880
      G  F  F  V  N  T  L  P  L  R  A  I  C  A  P  G  L  S  F  R

2881  GACCTGCTGGACCAGGTGCGCGAGGCCGCCCTCGGCGCCTTCGCCCATCAGGACCTCCCC  2940
      D  L  L  D  Q  V  R  E  A  A  L  G  A  F  A  H  Q  D  L  P

2941  TTCGAGGCGCTGGTCGAGGCGCTCGCACCCGAGCGCGACCTCGGCCACAATCCCCTCGTC  3000
      F  E  A  L  V  E  A  L  A  P  E  R  D  L  G  H  N  P  L  V

3001  CAGGTCACCTTCCAGCTCCTGGGCACACCGGCGGCGCGGCCGGACCTGATCGGGACGGAG  3060
      Q  V  T  F  Q  L  L  G  T  P  A  A  R  P  D  L  I  G  T  E

3061  GTCGAGCGGTACCCGGTCCAGGAGGCCGTCTCGCAGTTCGACCTGTCCCTGGACATCAAG  3120
      V  E  R  Y  P  V  Q  E  A  V  S  Q  F  D  L  S  L  D  I  K

3121  CGGGCCGACGACGGTTCCTACCGGGGGATCCTGAACTACTGCCCCGACCTGTTCGACCGA  3180
      R  A  D  D  G  S  Y  R  G  I  L  N  Y  C  P  D  L  F  D  R

3181  CGCCGCATGGAGGTGCTGGTCGGCCACTACCTGACGCTGCTCGGCGCCGCCGCCGCGGAC  3240
      R  R  M  E  V  L  V  G  H  Y  L  T  L  L  G  A  A  A  A  D

3241  CCGGGCCGCCCGATCGGTGAGCTGCCGCTGTCCGACGGGGCCGAACGGCTGCGGCTGCTC  3300
      P  G  R  P  I  G  E  L  P  L  S  D  G  A  E  R  L  R  L  L

3301  GACGGGTTCGGGAAGCGGGACGCGGCGTACGCCGGGCCGGGAAGCGTTCCGGAGCGGTTC  3360
      D  G  F  G  K  R  D  A  A  Y  A  G  P  G  S  V  P  E  R  F

3361  GCGGAGGTGGCGCGGACGGCACCGGACGCGCGGGCGGTGACGTGTGGCGCGACAACGCTC  3420
      A  E  V  A  R  T  A  P  D  A  R  A  V  T  C  G  A  T  T  L

3421  ACCTTCGCCGAGCTGAACGACCGGGTGGAGCGCCTGGCACAGGCACTGCTCGGCGCCGGG  3480
      T  F  A  E  L  N  D  R  V  E  R  L  A  Q  A  L  L  G  A  G

3481  GTCACCCGCGAGACGCCGGTCGCGGTCCGCCTGCCCCGTTCCACCGACAGCGTCGTCGCC  3540
      V  T  R  E  T  P  V  A  V  R  L  P  R  S  T  D  S  V  V  A

3541  CTGCTGGCCGTCATGCGGGCGGGCGGCGTCTACGTCCCCCTGGACCCCGACTGGCCCGCG  3600
      L  L  A  V  M  R  A  G  G  V  Y  V  P  L  D  P  D  W  P  A

3601  GACCGCACCGCCTACATCCTGGACGACACCGCGGCCTCCGTCGTCATCACCCGCGACCTG  3660
      D  R  T  A  Y  I  L  D  D  T  A  A  S  V  V  I  T  R  D  L

3661  CCCGCACTCCCCGGTCGCCTCCACGTCGACCCGCGCCGGCCCGCGGCCGACGGCCTGGTA  3720
      P  A  L  P  G  R  L  H  V  D  P  R  R  P  A  A  D  G  L  V

3721  CCCGCGCCCCGCATCGACCCCGATCAGGCCGCGTACGTCATCTACACGTCCGGCTCGACG  3780
      P  A  P  R  I  D  P  D  Q  A  A  Y  V  I  Y  T  S  G  S  T

3781  GGCGCGCCGAAGGGCGTCGTCGTCCGGCACCGCTCCCTGAACCACCTCACCAGCGCCCTG  3840
      G  A  P  K  G  V  V  V  R  H  R  S  L  N  H  L  T  S  A  L
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3841  CAGGCCACCTTTCTCGGCCACGACCCGTATCTCGCCGGGGCCGACGGCGTACCGCCCGGG  3900
      Q  A  T  F  L  G  H  D  P  Y  L  A  G  A  D  G  V  P  P  G

3901  GACGCGAAGCTGCGTACGACGCTCACCGCGCCCTTCACGTTCGACGCGTCCATGGAGCAA  3960
      D  A  K  L  R  T  T  L  T  A  P  F  T  F  D  A  S  M  E  Q

3961  CTGAGCTGGATGCTGGCCGGTCACGAGCTGTTCATCGTGCCCGAGGACGTGCGGCGCGAC  4020
      L  S  W  M  L  A  G  H  E  L  F  I  V  P  E  D  V  R  R  D

4021  CCCTCGGCGCTGGTCCGGTTCGTCCGGGAGCACCGGATCGACGTCATCGACACGACCTCC  4080
      P  S  A  L  V  R  F  V  R  E  H  R  I  D  V  I  D  T  T  S

4081  TCGCAGCTCGAACTCCTCGTATCGCACGGGCTGTTGGACGGAGAGTGGGCGCCGTCCATG  4140
      S  Q  L  E  L  L  V  S  H  G  L  L  D  G  E  W  A  P  S  M

4141  GTCATGGTGGGTGGCGAGGCGGTCTCGCCGTCGCTGTGGCGGACCTTGCGGGACCAGCGG  4200
      V  M  V  G  G  E  A  V  S  P  S  L  W  R  T  L  R  D  Q  R

4201  CGCACTCGCTGTTTCAACCTGTACGGGCCTACGGAGGCGACGGTCGACGCCACCTGCCAC  4260
      R  T  R  C  F  N  L  Y  G  P  T  E  A  T  V  D  A  T  C  H

4261  GACCTGTCCGACCCCGCCGACGTCCCCGTCATCGGCACCCCACTCCCCCACACCCACGTC  4320
      D  L  S  D  P  A  D  V  P  V  I  G  T  P  L  P  H  T  H  V

4321  CGCGTGCTCGACGACCGACTGCGACCCGTACCCGTGGGCGTCGCCGGCGAGATCTACCTC  4380
      R  V  L  D  D  R  L  R  P  V  P  V  G  V  A  G  E  I  Y  L

4381  GGCGGAACCGGCCTGGCCCGCGGCTACCTCAACCGCCCCGCCCTCACCGCCCGACGCTTC  4440
      G  G  T  G  L  A  R  G  Y  L  N  R  P  A  L  T  A  R  R  F

4441  GTCGCCGACCCCTACCCCGACACCCCCGGCAGCCGCCTGTACCGCACCGGCGACCGCGCC  4500
      V  A  D  P  Y  P  D  T  P  G  S  R  L  Y  R  T  G  D  R  A

4501  CGCTGGCGCCCCGACGGCACCCTCGAATACCTGGGACGCACCGACGACCAAATCAAGATC  4560
      R  W  R  P  D  G  T  L  E  Y  L  G  R  T  D  D  Q  I  K  I

4561  CGCGGCTTCCGCGTCGAACCCGGCGAAATCGAGGCCGTCCTCACCCACCACCCCGCCGTC  4620
      R  G  F  R  V  E  P  G  E  I  E  A  V  L  T  H  H  P  A  V

4621  AAGGAAGCCGCCGTCGTCGACGACGCGCACGCGCGGCTGGTCGCCTACGTCACGCTCGCG  4680
      K  E  A  A  V  V  D  D  A  H  A  R  L  V  A  Y  V  T  L  A

4681  GAAGGCGGCGGCGCCGGCCCCACCGACGTACGCCGGTTCGCGCAGGGGCGGCTGCCCGCC  4740
      E  G  G  G  A  G  P  T  D  V  R  R  F  A  Q  G  R  L  P  A

4741  CACATGGTGCCGTCGGCGGTGGTCGTCCTGGAGGCGCTGCCACTGACGTCGAACGGAAAG  4800
      H  M  V  P  S  A  V  V  V  L  E  A  L  P  L  T  S  N  G  K

4801  CTGGACCGCGCGCGCCTGCCGGCGCCCGCGGCGGGCAGACCGGAACTGGATGTCCGCTTC  4860
      L  D  R  A  R  L  P  A  P  A  A  G  R  P  E  L  D  V  R  F

4861  GTGGCGCCGCGCGACATGGTGGAGGAGGTCGTGGCGCAGGTCTGGTGCGCCGTGCTGGGC  4920
      V  A  P  R  D  M  V  E  E  V  V  A  Q  V  W  C  A  V  L  G

4921  GTCGACCGGGTCGGTGTGCACGACGACTTCTTCGAGCTGGGCGGGCACTCGTTGCTGGTG  4980
      V  D  R  V  G  V  H  D  D  F  F  E  L  G  G  H  S  L  L  V

4981  GTCCAGGTGATGACCCGGATACGAAAGCTGCTCGGCGTCGAGGTGCCGTTGCGGGAGCTG  5040
      V  Q  V  M  T  R  I  R  K  L  L  G  V  E  V  P  L  R  E  L

5041  TTCGACGCCGCGACGGTCGAGGAGCTCGCCGCCCGCGTCCGCGCCGCACGGACCGAGGGC  5100
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      F  D  A  A  T  V  E  E  L  A  A  R  V  R  A  A  R  T  E  G

5101  CTCGGCCGGGGGGCCGCCCCGCCCCTCGGGCCGGTGGACCGGAGCGGGCCGCTGCCGCTG  5160
      L  G  R  G  A  A  P  P  L  G  P  V  D  R  S  G  P  L  P  L

5161  TCGTTCGCGCAGCAACGCCTTTGGTACCTCGATCAGTTGGCGCCCGACAGTGTCTCCTAC  5220
      S  F  A  Q  Q  R  L  W  Y  L  D  Q  L  A  P  D  S  V  S  Y

5221  AACATGTGCGACGCCTACCGGGTCCGCGGCCCTCTCGACCTGGACGCGCTGCGGCGGGCG  5280
      N  M  C  D  A  Y  R  V  R  G  P  L  D  L  D  A  L  R  R  A

5281  CTGCGGACGCTGGTCGAGCGGCACGAGACGCTGCGGACGGCGTTCGTCGAGCGGGACGGG  5340
      L  R  T  L  V  E  R  H  E  T  L  R  T  A  F  V  E  R  D  G

5341  GTGCCCCACCAGGTGGTCTCGGCGCCCGACGCGCCGGCCGCGCGGCGCGCGGCGGAGGTC  5400
      V  P  H  Q  V  V  S  A  P  D  A  P  A  A  R  R  A  A  E  V

5401  GTGCGGATCGAGGCGGCCGGGCGGACCGACGAGGCGGTGCGGGACCTGGTGGCCGCGGAG  5460
      V  R  I  E  A  A  G  R  T  D  E  A  V  R  D  L  V  A  A  E

5461  GCGCGCACCCCGTTCCGGCCGGCGGACGGCGCGCTGATGCGCGTGGCGGTGGCCCGGCTG  5520
      A  R  T  P  F  R  P  A  D  G  A  L  M  R  V  A  V  A  R  L

5521  GCGGACGACGATCACGTGCTGGTGGTCACCACGCACCACATCGTCTCCGACGGCTGGTCG  5580
      A  D  D  D  H  V  L  V  V  T  T  H  H  I  V  S  D  G  W  S

5581  GTCGACATCCTGGTGGACGAATTGGGGCGCCTGTACCGGGAACACGTCACGGGTGACCCC  5640
      V  D  I  L  V  D  E  L  G  R  L  Y  R  E  H  V  T  G  D  P

5641  GCCGGGCTCCCTCCGCTCGACGTCCAGTACGCCGACTTCGCCGTCTGGCAGCGGTCCTGG  5700
      A  G  L  P  P  L  D  V  Q  Y  A  D  F  A  V  W  Q  R  S  W

5701  ATGACCGGCCCCGTGCGGGAGGAGCACCTCGCGTACTGGAAGCGGGCCCTGGACGGGGCA  5760
      M  T  G  P  V  R  E  E  H  L  A  Y  W  K  R  A  L  D  G  A

5761  CCCTCGGTCCTGCGGCTGCCGGCGGACCATCCGCGTCCCGCCGTCCAGTCCCAGCGGGGC  5820
      P  S  V  L  R  L  P  A  D  H  P  R  P  A  V  Q  S  Q  R  G

5821  GAGACCGTCGAGTTCCCCCTGCCCGCACCACTGGTCGCGCGGCTGGAAGCGCTCTGCCGG  5880
      E  T  V  E  F  P  L  P  A  P  L  V  A  R  L  E  A  L  C  R

5881  GAGCAGGGCGTCACCCTGTTCATGGCGCTCTTCGGCGCGTTCCAGGTGTTGCTGGCGCGC  5940
      E  Q  G  V  T  L  F  M  A  L  F  G  A  F  Q  V  L  L  A  R

5941  TACAGCGGTCAGGACGACGTGGTCGTGGGCGTGCCGACGGCGAACCGCACCCGCGCGGAG  6000
      Y  S  G  Q  D  D  V  V  V  G  V  P  T  A  N  R  T  R  A  E

6001  ACCGAGCCCCTGGTCGGCTTCTTCGTCAACACCCTTCCGGTACGGGTCGCGTGCTCGCCG  6060
      T  E  P  L  V  G  F  F  V  N  T  L  P  V  R  V  A  C  S  P

6061  GAGCTGTCGTTCCGCGCCCTGCTCGACCGGGTCCGCGAGGCCGCGCTGGGCGCCTTCGCC  6120
      E  L  S  F  R  A  L  L  D  R  V  R  E  A  A  L  G  A  F  A

6121  CATCAGGACCTGCCCTTCGAGGCGCTGGTCGAGGCGCTCGCGCCCGAGCGCGACCTGGGC  6180
      H  Q  D  L  P  F  E  A  L  V  E  A  L  A  P  E  R  D  L  G

6181  CACCACCCTCTCGTGCAGGTCACCTTCCAACTCCTCGACGCTCCCGACGAGAGGCTCGTC  6240
      H  H  P  L  V  Q  V  T  F  Q  L  L  D  A  P  D  E  R  L  V

6241  CTGCACGGCACGGACTGCGTCTCGCTCGGCTTCGGCGGTGTGACCAGCCGGTTCGACCTG  6300
      L  H  G  T  D  C  V  S  L  G  F  G  G  V  T  S  R  F  D  L
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6301  TCCCTCGACGTCGTCTCGGGGCGGCGGGGGAAGCGGTGCGTGCTGACGTACTGTCCCGAC  6360
      S  L  D  V  V  S  G  R  R  G  K  R  C  V  L  T  Y  C  P  D

6361  CTGTTCGACCGGCCCCGCATGGAGGTGCTGGCCGGCCACTACCTGACCCTGCTCGGCGCG  6420
      L  F  D  R  P  R  M  E  V  L  A  G  H  Y  L  T  L  L  G  A

6421  GCGGCCGACGATCCCGGTCTCCGCGTCGGCGACCTCCCGCTGAGCGACGACGTCGAACGC  6480
      A  A  D  D  P  G  L  R  V  G  D  L  P  L  S  D  D  V  E  R

6481  CTGCGCCTGCTGGGCGGGTCCCGCCCGCGGTACCTGCCCGCGCCCGGGGCGGAGACCGTC  6540
      L  R  L  L  G  G  S  R  P  R  Y  L  P  A  P  G  A  E  T  V

6541  CCTGACGCCTTCGCCGCGCAGGTGCGGGCGACACCGGACGCGCCCGCGCTGGTCCACGGG  6600
      P  D  A  F  A  A  Q  V  R  A  T  P  D  A  P  A  L  V  H  G

6601  GACTCGACGCTGACGTTCGCCGAGCTGGACACCCGGGTCACCGCCCTGGCCGTGCGGTTG  6660
      D  S  T  L  T  F  A  E  L  D  T  R  V  T  A  L  A  V  R  L

6661  CGGCGCTGCGGCGTGGCCGCCGAGACGCCGGTCGCGGTGTGCCTGCCGCGCTCCGCCGAC  6720
      R  R  C  G  V  A  A  E  T  P  V  A  V  C  L  P  R  S  A  D

6721  GCCGTCGTGGCCCTCCTGGCCGTCCTGCGGGCGGGCGGCGTCTATGTGCCAGTGGATCCG  6780
      A  V  V  A  L  L  A  V  L  R  A  G  G  V  Y  V  P  V  D  P

6781  GAGTGGCCCTCCGGCCGCGTCGCCCACGTCCTCGACGAGACCGCGGCCCCCGTCGTCATC  6840
      E  W  P  S  G  R  V  A  H  V  L  D  E  T  A  A  P  V  V  I

6841  ACCCGCGACCTGCCCGCCGATCCCGGCCGCGTCCACCTCGACCCGCGCCAGGCCCCGGCC  6900
      T  R  D  L  P  A  D  P  G  R  V  H  L  D  P  R  Q  A  P  A

6901  GACGACCGGGATCCCCTGCCGCGCCTCCACCGCGACCAGGCCGCGTACATCATCTTCACC  6960
      D  D  R  D  P  L  P  R  L  H  R  D  Q  A  A  Y  I  I  F  T

6961  TCGGGCTCCACCGGCGCCCCCAAGGGCGTCGTCGTCCGACACGGCTCCCTGTACCACCTC  7020
      S  G  S  T  G  A  P  K  G  V  V  V  R  H  G  S  L  Y  H  L

7021  CTGGGCCACGTACGGCGCATGGCGGAGGGCGGCCCCCGGCGGAACGTCGCGCACACCACC  7080
      L  G  H  V  R  R  M  A  E  G  G  P  R  R  N  V  A  H  T  T

7081  GCGATGACCTTCGACCCGTCGCTGGAACAGTTCCTGTGGCTCGTCGCCGGACACACCCTG  7140
      A  M  T  F  D  P  S  L  E  Q  F  L  W  L  V  A  G  H  T  L

7141  CACGTCGCGCCCGAGGAGGTGCGCCGCGATCCCGAGGCGCTGGTGGCCCTGGTGCGGCGC  7200
      H  V  A  P  E  E  V  R  R  D  P  E  A  L  V  A  L  V  R  R

7201  GCCGCGATCGACGTCCTCAACGTCACCCCGTCCCACCTGACCCTGCTGATCGAGGCCGGG  7260
      A  A  I  D  V  L  N  V  T  P  S  H  L  T  L  L  I  E  A  G

7261  CTGCTGGAGGGCGACCGGGTGCCGGGTACGGTCCTGGTGGGTGGCGAGGCGGTGCCCGCG  7320
      L  L  E  G  D  R  V  P  G  T  V  L  V  G  G  E  A  V  P  A

7321  GCGCTGTGGCGGACCCTGCGCGAACGGACGGGAGCCACCCGCTTCTTCAACCTGTACGGG  7380
      A  L  W  R  T  L  R  E  R  T  G  A  T  R  F  F  N  L  Y  G

7381  CCTACGGAGGCGACGGTCGACGCCACCTGCCACGACCTGTCCGACCCCGCCGACGTCCCC  7440
      P  T  E  A  T  V  D  A  T  C  H  D  L  S  D  P  A  D  V  P

7441  GTCATCGGCACCCCACTCCCCCACACCCACGTCCGCGTGCTCGACGACCGACTGCGACCC  7500
      V  I  G  T  P  L  P  H  T  H  V  R  V  L  D  D  R  L  R  P

7501  GTACCCGTGGGCGTCGCCGGCGAAATCTACCTCGGCGGAACCGGCCTGGCCCGCGGCTAC  7560
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      V  P  V  G  V  A  G  E  I  Y  L  G  G  T  G  L  A  R  G  Y

7561  CTCAACCGCCCCGCCCTCACCGCCCAACGCTTCGTCGCCGACCCCTACCCCGACACCCCC  7620
      L  N  R  P  A  L  T  A  Q  R  F  V  A  D  P  Y  P  D  T  P

7621  GGCAGCCGCCTGTACCGCACCGGCGACCGCGCCCGCTGGCGCCCCGACGGCACCCTCGAA  7680
      G  S  R  L  Y  R  T  G  D  R  A  R  W  R  P  D  G  T  L  E

7681  TACCTGGGACGCACCGACGACCAAATCAAGATCCGCGGCTTCCGCGTCGAACCCGGCGAG  7740
      Y  L  G  R  T  D  D  Q  I  K  I  R  G  F  R  V  E  P  G  E

7741  ATCGAAGCCGTCCTCACCCACCACCCCGCCGTCAAGGAAGCCGCCGTCACCGTGGCCACC  7800
      I  E  A  V  L  T  H  H  P  A  V  K  E  A  A  V  T  V  A  T

7801  GACGACGGTGCCGCCCGGCTGGTCGCCCTCGTCGTCCCCGCCCCCCGCGCCCCGCACGGC  7860
      D  D  G  A  A  R  L  V  A  L  V  V  P  A  P  R  A  P  H  G

7861  GATTCGGCCGACGGCGCCCCGGACGCCCAGGTCGAGGAGTGGAACGCCGTCTTCGAGGCG  7920
      D  S  A  D  G  A  P  D  A  Q  V  E  E  W  N  A  V  F  E  A

7921  ACCCACACCGACGCCGCCGACGGCGAACTCACCTTCAACATCAAGGGCTGGAACGACAGC  7980
      T  H  T  D  A  A  D  G  E  L  T  F  N  I  K  G  W  N  D  S

7981  CTCACCGGTGCGCCGATCCCCGCCGAACACATGCGGGAATGGGTCGACACCACCGTCGCC  8040
      L  T  G  A  P  I  P  A  E  H  M  R  E  W  V  D  T  T  V  A

8041  CGGCTCCTGGAACGGCCGGCCGAGCGCGTCCTGGAGATCGGCAGTGGCACCGGGCTGCTG  8100
      R  L  L  E  R  P  A  E  R  V  L  E  I  G  S  G  T  G  L  L

8101  ATGTGGCGGCTGCTGCCGCACGTCACCGAGTACACCGGAACCGACTTCTCGCGGCCCGCC  8160
      M  W  R  L  L  P  H  V  T  E  Y  T  G  T  D  F  S  R  P  A

8161  GTGGACTGGCTCCGGGACGGGCTGCGCCGCCGCCCCGCGCACCGGGTACGGCTGCTGCAC  8220
      V  D  W  L  R  D  G  L  R  R  R  P  A  H  R  V  R  L  L  H

8221  CGCGAGGCGACCGACTTCACCGGCGTCCGCGCCGCGTCCACCGACCTCGTCGTCGTCAAC  8280
      R  E  A  T  D  F  T  G  V  R  A  A  S  T  D  L  V  V  V  N

8281  TCGGTCGTCCAGTACTTCCCCGACCGCGCCTACCTCGACACCGTCCTGGCCCGCGCCCTC  8340
      S  V  V  Q  Y  F  P  D  R  A  Y  L  D  T  V  L  A  R  A  L

8341  GACGCCACGGCCGACCGAGGGCGCGTCTTCGTGGGCGACGTGCGCAACCTGGCCCTCGCC  8400
      D  A  T  A  D  R  G  R  V  F  V  G  D  V  R  N  L  A  L  A

8401  CCGCAGTTCTACGCCCGTCAGGCCCTCGCCCACGCCGGTCCGGGCGCGGCGGCGCGGGAC  8460
      P  Q  F  Y  A  R  Q  A  L  A  H  A  G  P  G  A  A  A  R  D

8461  GTGGCGCGCGCCGCCGGCGAGTTCGCGGCCATGGACGGCGAGTTGCTGGTGTCCCCCGCG  8520
      V  A  R  A  A  G  E  F  A  A  M  D  G  E  L  L  V  S  P  A

8521  TACTTCGCCGCGCTCGCCGCCCGCTCGCCCCGCGTCACCGGCGTCGAGATCCTGCCCCGC  8580
      Y  F  A  A  L  A  A  R  S  P  R  V  T  G  V  E  I  L  P  R

8581  CGGGGACGGCACCGCAACGAGATGAGCCTGTACCGCTACGACGTGGTGCTGCACGTGGGC  8640
      R  G  R  H  R  N  E  M  S  L  Y  R  Y  D  V  V  L  H  V  G

8641  GGTGACCGCCCGGCGGCCCCGGAGGCGGAGGTGCTCACCTGGGGCGACCAGGTGCACGAC  8700
      G  D  R  P  A  A  P  E  A  E  V  L  T  W  G  D  Q  V  H  D

8701  CTCGCGTCGCTGTCCGCCCGCCTCGGCCGCGGGGGCCCGGACGCCCTGCTCGTGCGCGGC  8760
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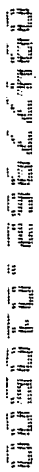

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8761  GTCGCCAACGACCGTCTGACGCGGGACAACGAGCTGCTCGACGCACCCGCCCGCACGACG  8820
      V  A  N  D  R  L  T  R  D  N  E  L  L  D  A  P  A  R  T  T

8821  GCCGTCGAGCCCGAGGACCTGTGGGGGCTGGCGGACTCCACCCCCTACCGGGTGAGCGTC  8880
      A  V  E  P  E  D  L  W  G  L  A  D  S  T  P  Y  R  V  S  V

8881  AGCTGGGCCGCCGCCGATCCGCGGGGCGCGATGGACGTCCTGCTGGTCCGGCGGGACGCC  8940
      S  W  A  A  A  D  P  R  G  A  M  D  V  L  L  V  R  R  D  A

8941  CACGACGACGGTCCGCTGCTCGTCCCCCACCCCGTACCGGAGCCCTCGGCACCGCTGACG  9000
      H  D  D  G  P  L  L  V  P  H  P  V  P  E  P  S  A  P  L  T

9001  AACACGCCGACCCGGCACCCGTCCGCGCGGCAAGGGGGCTCGGCCGCGGACGGGCTGCGT  9060
      N  T  P  T  R  H  P  S  A  R  Q  G  G  S  A  A  D  G  L  R

9061  TCCTGGCTCGCCGAGCGGCTTCCCGCGCACCTGCTGCCCGCGAGGATCACCGAGGTGGAC  9120
      S  W  L  A  E  R  L  P  A  H  L  L  P  A  R  I  T  E  V  D

9121  GCGCTGCCCCGCACCGGCACCGGCAAGCTCGACCGGGGCGCGCTCGGCGGACTCGTGACC  9180
      A  L  P  R  T  G  T  G  K  L  D  R  G  A  L  G  G  L  V  T

9181  GCGGGCCGTGGCGCCCGGGCGGGCGACCGCCCCGCCACCGCCCCCCGTACGGGTCTCGAA  9240
      A  G  R  G  A  R  A  G  D  R  P  A  T  A  P  R  T  G  L  E

9241  CGGACCCTGGCCGACGCGTGGGCGCGGGTGCTCGGCCTCCCCGAAGTCGGCGTGCACGAG  9300
      R  T  L  A  D  A  W  A  R  V  L  G  L  P  E  V  G  V  H  E

9301  AACTTCTTCGCCCTCGGCGGCGACTCCCTCCTCGCCGTCAGGGCTGTCGCCCGGTGCCGC  9360
      N  F  F  A  L  G  G  D  S  L  L  A  V  R  A  V  A  R  C  R

9361  CGTGCCGGGGTCCGACTGACCGTCCGGCAGTTGCTGAGCGAGCAGACCGTCGCCGCGCTC  9420
      R  A  G  V  R  L  T  V  R  Q  L  L  S  E  Q  T  V  A  A  L

9421  GCGGCGGCCCTCGAGGAGGAGTCTCAATGATGAAGTCAAGCCGCTTGCGCGACCGGCAGC  9480
      A  A  A  L  E  E  E  S  Q  *
                                 M  M  K  S  S  R  L  R  D  R  Q  L
                                 (orf33)

9481  TCGGGGGTGAAGACCCGGTTGTCGCGCAGGAGAGCCCACAGGACGCTGGCCCGACGCCGT  9540
        G  G  E  D  P  V  V  A  Q  E  S  P  Q  D  A  G  P  T  P  C

9541  GCCAGGGCGATGACGGCTTGAACGTGTTTGCAGCCCTCGCCGCGCTTCTTGAGGTAGAAG  9600
        Q  G  D  D  G  L  N  V  F  A  A  L  A  A  L  L  E  V  E  V

9601  TCCCGGTTCGGCCCCTCCCGCATCATGCTGGTTTGGGCCGACATGTAGAACACTCGTCGC  9660
        P  V  R  P  L  P  H  H  A  G  L  G  R  H  V  E  H  S  S  Q

9661  AGGCGGCGGCTGTAGCGCTTGGGCCGATGCAGGTTGCCAGTGCGACGACCGGAGTCGCGG  9720
        A  A  A  V  A  L  G  P  M  Q  V  A  S  A  T  T  G  V  A  G

9721  GGGACGGGCACCAGGCCGGCCGCCGAGGCCAGGTGACCGGCGTCGGCGTAGGCCGTGAGG  9780
        D  G  H  Q  A  G  R  R  G  Q  V  T  G  V  G  V  G  R  E  V

9781  TCGCCGGCGGCGACGACGAACTCGGCGCCGAGGATCGGCCCCATGCCCGGCAGAGACTCG  9840
        A  G  G  D  D  E  L  G  A  E  D  R  P  H  A  R  Q  R  L  D

9841  ATGATCTCGGCCTGTGGATGGCTGCGGAACGTCTCGCGGATCTGCTGGTCAATCCGCTTC  9900
        D  L  G  L  W  M  A  A  E  R  L  A  D  L  L  V  N  P  L  Q

9901  AGACGGTCGTCCAGGGCCAGGATCTGCGCGGCCAGGTCAGCCACGATCTGGGCGGCGACG  9960
        T  V  V  Q  G  Q  D  L  R  G  Q  V  S  H  D  L  G  G  D  V
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9961  TCCTCCCCGGGCAGCGCGGTCTGCTGAGCCTGGGCAGCCTCCAGCGCCGTCGCGGCGACG  10020
        L  P  G  Q  R  G  L  L  S  L  G  S  L  Q  R  R  R  G  D  G

10021 GCGTCGGCACCGCGCACGCCTCGGTTGGCCAGCCAGGCCGTCAGCCGGGCCCGGCCGCGG  10080
        V  G  T  A  H  A  S  V  G  Q  P  G  R  Q  P  G  P  A  A  A

10081 CGGCGGAGAGCTGCCGGGGTCTGGTAGCCCGTCAGCAGGACCAGCGCGCCCTTCTGCGAG  10140
        A  E  S  C  R  G  L  V  A  R  Q  Q  D  Q  R  A  L  L  R  A

10141 CTGTAGTCGAAGGCCCGTTCCAGCGCGGGGAAGACGCCGGTCAGCGTGTCGCGGAGACGG  10200
        V  V  E  G  P  F  Q  R  G  E  D  A  G  Q  R  V  A  E  T  V

10201 TTGATCATCCTGACCCGGTCGGCCACGAGGTCGGAACGGTGGGCGGTCAGCAGCGCGAGG  10260
        D  H  P  D  P  V  G  H  E  V  G  T  V  G  G  Q  Q  R  E  V

10261 TCGGCGGCCAGCTGGGCGGGCACGTCGATCGACGCGAAGTCCCGTCGGTTGCGGGCGGTT  10320
        G  G  Q  L  G  G  H  V  D  R  R  E  V  P  S  V  A  G  G  F

10321 TCGGCGATGACGTAGGCGTCGCGGGCGTCGGTCTTCGCCTCGCCCCGGTAAGCGCCGGAC  10380
        G  D  D  V  G  V  A  G  V  G  L  R  L  A  P  V  S  A  G  H

10381 ATGCGGTTGACCGTGCGGCCGGGCACGTAGACGGCCTGCTGGCCGTGGGCCGCGAGCAGG  10440
        A  V  D  R  A  A  G  H  V  D  G  L  L  A  V  G  R  E  Q  G

10441 GCCAGCAGCAGCGCGGAGGACGTGCCGGAGATGTCCACTGCCCAGTGGACCTCGTCGGCC  10500
        Q  Q  Q  R  G  G  R  A  G  D  V  H  C  P  V  D  L  V  G  Q

10501 AGGTCGAGGATCTCACCCATGGCGGTCAGGATCGCCGACTCATCGTTGCCGATCTTCTTC  10560
        V  E  D  L  T  H  G  G  Q  D  R  R  L  I  V  A  D  L  L  R

10561 GACCACAGCGTCACACCGGTCTCGTCGACCACCGCCGCCCAGTGATGCCCCTTGCCCGCG  10620
        P  Q  R  H  T  G  L  V  D  H  R  R  P  V  M  P  L  A  R  V

10621 TCGATCCCGGCCCAGACCCGGGCCCGTCGCTCGCCCACTCGCCCCTCCTCACTCCGAACA  10680
        D  P  G  P  D  P  G  P  S  L  A  H  S  P  L  L  T  P  N  S

10681 GCATCCCGTCGACCCGAGGAACACCCCGCTGTCATCTCCGTAAAAAGCGACCGAAGCGCA  10740
        I  P  S  T  R  G  T  P  R  C  H  L  R  K  K  R  P  K  R  T

10741 CATCTCAATCAGCAGCCAGGGCGCCCCGGAGAACCGGGCGGCCACTCCTTGTAAGCCACT  10800
        S  Q  S  A  A  R  A  P  R  R  T  G  R  P  L  L  V  S  H  *

10801 GACGGCAGAGAACCATAAGCCACACCCGGCCCTCCCGGGCCGCCTAACAACTTACGGAGA  10860

10861 ACCATGACTGACCTGCCGTTGCGTACCGTCGCACTCACCGGTGAGGAGAGCGCGGAGGTC  10920
          M  T  D  L  P  L  R  T  V  A  L  T  G  E  E  S  A  E  V
          (orf34)

10921 GACGACCTGCTGCGCACGCTGGCCGACGTGCCGGTCGACTCCACCGTGGGACTGCTGCAC  10980
        D  D  L  L  R  T  L  A  D  V  P  V  D  S  T  V  G  L  L  H

10981 CGCACCCGGCTCGCCGCACAGGAACTGCCGCTGCGCATCCGCGCCGAGCTCACGGGGATG  11040
        R  T  R  L  A  A  Q  E  L  P  L  R  I  R  A  E  L  T  G  M

11041 CGGCTCTACGACAGCCCGCGCGCCCTCGTCGTCACGGGCTTCGGCGTCGACGACGAACGG  11100
        R  L  Y  D  S  P  R  A  L  V  V  T  G  F  G  V  D  D  E  R

11101 ATCGGACCGACCCCCGCGGCCCGTCCCGCCCCGGATCCCGAGCGGACCCGCGACCTGGAG  11160
        I  G  P  T  P  A  A  R  P  A  P  D  P  E  R  T  R  D  L  E

11161 CTGCTGCTTTTGCTGCACGCGGCCCTGCTCGGCGAGGCGTTCGGCTGGGCGACCCAGCAG  11220
        L  L  L  L  L  H  A  A  L  L  G  E  A  F  G  W  A  T  Q  Q
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11221  AACGGCCGGCTCGTCCACGACGTGCTGCCCGTTCCCGGTGAGGAGACCGCGCAGATGGGT  11280
       N  G  R  L  V  H  D  V  L  P  V  P  G  E  E  T  A  Q  M  G

11281  TCCAGCAGCGAGACCGAGCTGCTGTGGCACACCGAGGACGCGTTCCACCCGCTGCGCTGC  11340
       S  S  S  E  T  E  L  L  W  H  T  E  D  A  F  H  P  L  R  C

11341  GACTACGTGGGCCTGCTGTGCCTGCGCAACCACCAGCGCGCCGCGACCACCGTGGGCTGG  11400
       D  Y  V  G  L  L  C  L  R  N  H  Q  R  A  A  T  T  V  G  W

11401  CCCGACCTGTCCCGGCTCACCACCGAGGACCGTGCCGTGCTCCTCGAACCCCGCTATCTG  11460
       P  D  L  S  R  L  T  T  E  D  R  A  V  L  L  E  P  R  Y  L

11461  ATCCGCCCGGACACCTCGCACACGCCCGCGCAGAACGCGACGGGCACGCGGTCCGCCGAG  11520
       I  R  P  D  T  S  H  T  P  A  Q  N  A  T  G  T  R  S  A  E

11521  CGTTTCGCGGCGATCGCCGAGATGGACGACGCCCCGGAGCGCGTCGCCGTCCTGTTCGGC  11580
       R  F  A  A  I  A  E  M  D  D  A  P  E  R  V  A  V  L  F  G

11581  GACCCCGAGGACCCGTACCTGCGGATCGACCCGGCCTACATGAGCCCGGCCCCCGGGGAC  11640
       D  P  E  D  P  Y  L  R  I  D  P  A  Y  M  S  P  A  P  G  D

11641  GCGGCCGCCCGGCGGGCGTACGACACCGTCACCGCGCTCATCGAGGACGAGCTGCGGCAC  11700
       A  A  A  R  R  A  Y  D  T  V  T  A  L  I  E  D  E  L  R  H

11701  GTCGTCCTGGACGCCGGTTCACTGCTGCTGGTCGACAACTACCAGGCGGTGCACGGCCGC  11760
       V  V  L  D  A  G  S  L  L  L  V  D  N  Y  Q  A  V  H  G  R

11761  AAGCCGTTCGCCGCCGCCTACGACGGCCGCGACCGCTGGCTCAAACGCGTCAACATCACC  11820
       K  P  F  A  A  A  Y  D  G  R  D  R  W  L  K  R  V  N  I  T

11821  CGCGACCTGCGCCGTTCCCGGTCCGCGCGGCGGTCGGCCACCTCGCTGCTGGTGTGAGGG  11880
       R  D  L  R  R  S  R  S  A  R  R  S  A  T  S  L  L  V  *

11881  AGGCACCATGGATTTCCCCCTCACCCGCGTCAACCCCTGGTTCAGCGGCGGCTGCGACGG  11940
              M  D  F  P  L  T  R  V  N  P  W  F  S  G  G  C  D  G
              (orf35)

11941  CCGCCCCCGGGTGCGGCTGTGCGCGCTGCCGTACGCGGGCGGCACCGCCGCCGTCTTCAA  12000
        R  P  R  V  R  L  C  A  L  P  Y  A  G  G  T  A  A  V  F  K

12001  GGACTGGCCCGCCGCGCTGCCCCCCGGAGTGGAGCTGCTCACCGCGCACCTGCCGGGACG  12060
        D  W  P  A  A  L  P  P  G  V  E  L  L  T  A  H  L  P  G  R

12061  CGGCGACCGGTTCACCGAACCGCCCCCGGCCACCCTGGAGGAGACCGCCGAGCGGCTGTG  12120
        G  D  R  F  T  E  P  P  P  A  T  L  E  E  T  A  E  R  L  C

12121  CGAGGCGCTGCCGCCGAGTGACCTGCCCACGGTCGTCCTCGGCCACAGCATGGGCGCCCT  12180
        E  A  L  P  P  S  D  L  P  T  V  V  L  G  H  S  M  G  A  L

12181  GCTGGGGTACGAAGTGGCGGCGCGGCTCGCGGCGCGGGGCCGCGCCCCCAACCTGCTGAT  12240
        L  G  Y  E  V  A  A  R  L  A  A  R  G  R  A  P  N  L  L  I

12241  CGCCGCGGCCTGCCGTCCCCCGCACGTTCCGCCGGACGCCTCCGGTCCGGTGACCGAGGC  12300
        A  A  A  C  R  P  P  H  V  P  P  D  A  S  G  P  V  T  E  A

12301  CGAGCTGGCGGCCACCCTGCGGGCCGAACGCCCATGGGACACGGCCCTGAGGGACGAGGA  12360
        E  L  A  A  T  L  R  A  E  R  P  W  D  T  A  L  R  D  E  E

12361  ACTGATGGAAGCGGTGCTGCCCGCCCTGGTCGCCGACATCACGGCCGGCGACCGCTACCA  12420
        L  M  E  A  V  L  P  A  L  V  A  D  I  T  A  G  D  R  Y  H

12421  CCGCCCGCGGCCCCGCCCGCTCGACCTCCCGCTGAAGGTCTACATCGGCGCCGACGACGA  12480
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                R  P  R  P  R  P  L  D  L  P  L  K  V  Y  I  G  A  D  D  D

12481  CGGCACCGACTGGCGCACCACCCTGGGCTGGCGCGCGTGCACCGCCCGGGACTGCGAGGT  12540
         G  T  D  W  R  T  T  L  G  W  R  A  C  T  A  R  D  C  E  V

12541  CGTCGTCCTGCCCGGCGGCCACTACTTCCTGGAGACCGACCGCGCGGCCGTCCTCACCCG  12600
         V  V  L  P  G  G  H  Y  F  L  E  T  D  R  A  A  V  L  T  R

12601  CGTCGCCACGGACCTCGCCGAAGCCGAGGTAGGGGCATGACCGCGCGCGTCGACGCCACA  12660
         V  A  T  D  L  A  E  A  E  V  G  A  *
                                          M  T  A  R  V  D  A  T
                                         (orf36)

12661  CCCACCTACCTGGCGGTGCTGGCGGTGCGCGAGGCCCGCGCCCCGCTCCTCGGCAGCTGC  12720
         P  T  Y  L  A  V  L  A  V  R  E  A  R  A  P  L  L  G  S  C

12721  CTGGCCCGCATGTCCTTCGCGGTGCTGCCGCTCGCCCTGCTGCTGTCGGTCCGGGACGCG  12780
         L  A  R  M  S  F  A  V  L  P  L  A  L  L  L  S  V  R  D  A

12781  ACGGGGTCGTTCGCCGTCGCCGGACTGACCTCCGGCGCGCTGTCGGCCACGCTCACGCTG  12840
         T  G  S  F  A  V  A  G  L  T  S  G  A  L  S  A  T  L  T  L

12841  TTCGCGCCCGCCCGCGCCCGGCTGATCGACCGCCGGGGCTCACGGTCCGGACTGGTCCGG  12900
         F  A  P  A  R  A  R  L  I  D  R  R  G  S  R  S  G  L  V  R

12901  CTGACCGTCCCGTACCTGCTGGGGCTCGCCGTGCTGATCACATTGGCCGAGGCGGAAGCG  12960
         L  T  V  P  Y  L  L  G  L  A  V  L  I  T  L  A  E  A  E  A

12961  CCCACCGCGGCGCTGCTCGTCGCCGCCGCGGTCGCGGGCGTGTTCGCGCCGCCGCTCGGT  13020
         P  T  A  A  L  L  V  A  A  A  V  A  G  V  F  A  P  P  L  G

13021  CCGACCATGCGCGTGCTGTGGGCGAGGATCCTGCACGGCCGTCAGCCCCTGCTGCACACC  13080
         P  T  M  R  V  L  W  A  R  I  L  H  G  R  Q  P  L  L  H  T

13081  GCCTACGCCCTCGACTCCGTCACCGAGGAGGTGGTCTTCACCGTGGGGCCGCTGCTGGCG  13140
         A  Y  A  L  D  S  V  T  E  E  V  V  F  T  V  G  P  L  L  A

13141  GGCGGCCTGATCGCGGTCGCGGCACCGCTCGCGTCGATGATCACGGTCATGGTGCTGATC  13200
         G  G  L  I  A  V  A  A  P  L  A  S  M  I  T  V  M  V  L  I

13201  GCGGCCGGTACCGCCTGCTTCGTGCTGTCCGCCGCGACCGCCGCCGCCCCCGCGTCGGGC  13260
         A  A  G  T  A  C  F  V  L  S  A  A  T  A  A  A  P  A  S  G

13261  GAAGCCGACGAGGACCGGCCGCACGGCCGGCCCATGGCTCTGCCCGGGATGCGCACGATC  13320
         E  A  D  E  D  R  P  H  G  R  P  M  A  L  P  G  M  R  T  I

13321  GTGCTGTCCTTCGGCGGCGTCGGCCTGGTCGTCGGGGTGCTCCAGGTCGTCCTGCCGTTC  13380
         V  L  S  F  G  G  V  G  L  V  V  G  V  L  Q  V  V  L  P  F

13381  ATCGCCGACCACGCGGGCTCGCCCGGCGCGGGCGGCATCCTGCTGTCCATGCTGTCGGCG  13440
         I  A  D  H  A  G  S  P  G  A  G  G  I  L  L  S  M  L  S  A

13441  GGCAGCGCGGTCGGCGGCCTCGCCTACGGGCGGATCGCCTGGCGCTCGACGCCCGTGCGG  13500
         G  S  A  V  G  G  L  A  Y  G  R  I  A  W  R  S  T  P  V  R

13501  CGGTTCGTGGTGCTCGTCACCGGGTTCACGCTGGCGGTGCTGCCGCTGTGCCTGACCGCG  13560
         R  F  V  V  L  V  T  G  F  T  L  A  V  L  P  L  C  L  T  A

13561  AGCCCGGTGCCGGCCGGGGCCTTCGCCCTCCTCGTGGGACTCTGCCTCGCCCCGCTGTTC  13620
         S  P  V  P  A  G  A  F  A  L  L  V  G  L  C  L  A  P  L  F

13621  ACCACCGCCTACCTGCTGGTCAACGACCTGGTGACGGCGTCGGGGACCGCACCCACCGAG  13680
         T  T  A  Y  L  L  V  N  D  L  V  T  A  S  G  T  A  P  T  E
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13681  GCCAACACCTGGGTCTCCACGGCCAATAACGGAGGGTTCGCCGCGGGCAGCGCCGCCGCC  13740
       A  N  T  W  V  S  T  A  N  N  G  G  F  A  A  G  S  A  A  A

13741  GGTGTGCTGCTCGACTCCCGGGGCCCCACCGTCACCGTCACCGCCGCGTTCGCGGTCGCC  13800
       G  V  L  L  D  S  R  G  P  T  V  T  V  T  A  A  F  A  V  A

13801  GCCGCGACCGCCGTCATGACCGTTCTGCGCCGCCGGACCCTGCTCCTCGGCGCCGGACAC  13860
       A  A  T  A  V  M  T  V  L  R  R  R  T  L  L  L  G  A  G  H

13861  CCCGAACCGGCCGCCGCCACACCCGCCGACCGCACCGCACCCGCCGAAGCCGAGGAGTGA  13920
       P  E  P  A  A  A  T  P  A  D  R  T  A  P  A  E  A  E  E  *

13921  ACCGATCGTGTCCAAGAACGCGGCGCACTGGTCGCGCATCCGCACAGGGGACGCCCCCGG  13980
             M  S  K  N  A  A  H  W  S  R  I  R  T  G  D  A  P  G
            (orf37)

13981  CGTCGTACTCGCCGTGGACTTCTACGGAACGGGCCGCCAGGAAGCCACCTTCCGCCACCT  14040
       V  V  L  A  V  D  F  Y  G  T  G  R  Q  E  A  T  F  R  H  L

14041  GTGCGACCTGCTCACGGATCCGGTCGAGGTCTGGCACGCGGTCCCGCCCGCCCCGGACGG  14100
       C  D  L  L  T  D  P  V  E  V  W  H  A  V  P  P  A  P  D  G

14101  CGACTGGTCCACGGCCACCGGCGCCGGTCACCTGCGCTGGTGGACCGAGGGGCTCGACAC  14160
       D  W  S  T  A  T  G  A  G  H  L  R  W  W  T  E  G  L  D  T

14161  GGTCCTCGCGGGACGGCCGGTGCGGGCCCTCGTCGGCTACTGCGCGGGCGGCGTCTTCGC  14220
       V  L  A  G  R  P  V  R  A  L  V  G  Y  C  A  G  G  V  F  A

14221  CTCGGCCCTCGCCGACGCCCTCGTCGAACGGGAGGGCCACCGGCCGCGGGTCGTGCTGTT  14280
       S  A  L  A  D  A  L  V  E  R  E  G  H  R  P  R  V  V  L  F

14281  CAACCCCAGCGCGCCCGGCGTCGCCACGCTCACCCGCGACTTCCGCGGTCTGATCGCCGG  14340
       N  P  S  A  P  G  V  A  T  L  T  R  D  F  R  G  L  I  A  G

14341  CATGGACCTCCTCACGGACGGGGAACGCGCCGCTCTGCTGGCCGAGACGACCGCGATCCG  14400
       M  D  L  L  T  D  G  E  R  A  A  L  L  A  E  T  T  A  I  R

14401  GCGGGCACACGCCCCCGACGCGCTGGTACCGGTCGCCGAACGCTACGCCGCCCTGTACCG  14460
       R  A  H  A  P  D  A  L  V  P  V  A  E  R  Y  A  A  L  Y  R

14461  CGAGGGCTGCGACCTCCTGTGCGAGCGGCTCGGCGTGGACGCCTCCTTCGGCGCCGAACT  14520
       E  G  C  D  L  L  C  E  R  L  G  V  D  A  S  F  G  A  E  L

14521  GGCCGCCGTCCTCCACTCCTACCTGGCCTACCTCACGGCGGCGCTCGACGTGCCCCCCAC  14580
       A  A  V  L  H  S  Y  L  A  Y  L  T  A  A  L  D  V  P  P  T

14581  CCCGCTGTGGCGCGGCGCCGTCTCGCTCACCTCCCGCGAGCACCAGGGCACCGACTTCAC  14640
       P  L  W  R  G  A  V  S  L  T  S  R  E  H  Q  G  T  D  F  T

14641  CGACGTCGAGCACGGCTTCGACGTCGCCCGTGCCGAACTGCTGAGCTCCCCCCAGGTCGT  14700
       D  V  E  H  G  F  D  V  A  R  A  E  L  L  S  S  P  Q  V  V

14701  CGCGGCGCTGACCGCGCTCCTCCGCGAACACGAGGCGAGCCGATGACCCTCACCCTGCGG  14760
       A  A  L  T  A  L  L  R  E  H  E  A  S  R  *
                                                  M  T  L  T  L  R
                                                 (orf38)

14761  GACGCCTTCCTCGACCAGGCCGCCCGGACCCCCGACGCCCACGCCGTCGTACACGGCGAC  14820
       D  A  F  L  D  Q  A  A  R  T  P  D  A  H  A  V  V  H  G  D

14821  ACTGTATGGACGTACCGCGAACTGGAACTGCGGGCCGGCCGCATGGCCCGGACGCTGGCC  14880
       T  V  W  T  Y  R  E  L  E  L  R  A  G  R  M  A  R  T  L  A
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14881  GCACGCGGCGCGGGCCCCGGCACGCTGGTGGCGGTACGCCTGCCGCGCGGTCCCGAACCG  14940
       A  R  G  A  G  P  G  T  L  V  A  V  R  L  P  R  G  P  E  P

14941  GTCGCCGCGCTCCTCGCGGTCGTGCTGACGGGAGCGGGCTACGTGCCGCTCGCCGACGAC  15000
       V  A  A  L  L  A  V  V  L  T  G  A  G  Y  V  P  L  A  D  D

15001  GACCCGCCGGACCGGTGCCGGCACATCCTCGACGACTGCGCCGCCGCGCTGCTGCTGGCC  15060
       D  P  P  D  R  C  R  H  I  L  D  D  C  A  A  A  L  L  L  A

15061  GAGCACCCCTCGCGGGACGGACGCACCCTCACCCCGGACGAGGCGCTGGCACCCGCCCGC  15120
       E  H  P  S  R  D  G  R  T  L  T  P  D  E  A  L  A  P  A  R

15121  CCGTTCGACGCGGCCCCGGTGCGGGCCGGCGACCCGGCGTACGTGATCTACACCTCCGGC  15180
       P  F  D  A  A  P  V  R  A  G  D  P  A  Y  V  I  Y  T  S  G

15181  TCCAGTGGCCGTCCGAAGGGCGTGCTGGTCGAACAGGGCGCGCTCGGCGCCTACCTGGCA  15240
       S  S  G  R  P  K  G  V  L  V  E  Q  G  A  L  G  A  Y  L  A

15241  CAGGCCCGCGCGCGCTACGACGGGCTGTCCGGACGGACGGTGCTGCACTCCTCGCTGTCC  15300
       Q  A  R  A  R  Y  D  G  L  S  G  R  T  V  L  H  S  S  L  S

15301  TTCGACATGGCCGTGACCAGTCTGTGGGGCCCGCTCGTCAGCGGCGGCGCGATCCACGTG  15360
       F  D  M  A  V  T  S  L  W  G  P  L  V  S  G  G  A  I  H  V

15361  CTCGACCTGAAGGCGATCGCCTCCGGCACCCAGCCGCCGCCCGCCGCCTCGGCACGTCCG  15420
       L  D  L  K  A  I  A  S  G  T  Q  P  P  P  A  A  S  A  R  P

15421  TCCTTCCTCAAGGTCACTCCGTCCCACCTGCCGCTGCTGGGCCTGCTGCCGGACTCCTGC  15480
       S  F  L  K  V  T  P  S  H  L  P  L  L  G  L  L  P  D  S  C

15481  CTGCCCACCGGGCAACTCGTGATCGGCGGCGAGGCGCTGACCGGCTCCGCGCTCGGACCC  15540
       L  P  T  G  Q  L  V  I  G  G  E  A  L  T  G  S  A  L  G  P

15541  TGGCGCGCCGCGCACCCCGACGTCACGGTCGTCAACGAGTACGGGCCCACCGAGGCGACC  15600
       W  R  A  A  H  P  D  V  T  V  V  N  E  Y  G  P  T  E  A  T

15601  GTCGGCTGCTGCGCGTACACCGTCCGCCCCGGTGACGCCGTGGACCCGGGTGCCGTCCCC  15660
       V  G  C  C  A  Y  T  V  R  P  G  D  A  V  D  P  G  A  V  P

15661  ATCGGACGGCCGTTCGCGGGCACCCGCCTGTACGTGCTCGACGCGGACGGCGAGCCGGTC  15720
       I  G  R  P  F  A  G  T  R  L  Y  V  L  D  A  D  G  E  P  V

15721  GCCGTGGGCGGTGTGGGTGAACTGCACATCGCGGGCGACCAGTTGGCGCGCGGATACCTG  15780
       A  V  G  G  V  G  E  L  H  I  A  G  D  Q  L  A  R  G  Y  L

15781  GGGCGCCCGCGGCTGACCGAGGAACGCTTCGTCCCGGACCCGTTCGCCGCCGACGGCTCC  15840
       G  R  P  R  L  T  E  E  R  F  V  P  D  P  F  A  A  D  G  S

15841  CGGATGTACCGCACCGGCGACCTGGTGCGCGAACGCCCGGACGGCGACCTGGAGTACCTC  15900
       R  M  Y  R  T  G  D  L  V  R  E  R  P  D  G  D  L  E  Y  L

15901  GGGCGCGCGGACGGGCAGGTGAAGGTCTCCGGGTACCGGATCGAGCCCGGCGAGATCGAG  15960
       G  R  A  D  G  Q  V  K  V  S  G  Y  R  I  E  P  G  E  I  E

15961  GCCGTGCTCCGCGGCCACGCGGGGGTGAGGGACTGCGCGGTCGTCGCCGTCGGCGAGGCG  16020
       A  V  L  R  G  H  A  G  V  R  D  C  A  V  V  A  V  G  E  A

16021  GACGCCCGCCGGCTCGTCGCCTACGTGGTACCGGACCCGGACTCCCCGCCCGGCACCGCC  16080
       D  A  R  R  L  V  A  Y  V  V  P  D  P  D  S  P  P  G  T  A

16081  GCGCCGGCGCGGCACGCGGCCGAGGCGCTGCCGCCGTACATGGTGCCGGCGACGTTCGTC  16140
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      A  P  A  R  H  A  A  E  A  L  P  P  Y  M  V  P  A  T  F  V

16141 ACCGTGCCCGAACTGCCGCTCACCCCCAACGGGAAGCTCGACCGGGACGCGCTGCCCGGC 16200
      T  V  P  E  L  P  L  T  P  N  G  K  L  D  R  D  A  L  P  G

16201 CCCCCTGCCGGCGACGCCGGGCCGGGCGACCGCACCCCGGCCGAGACCCTGCTGTGCGAG 16260
      P  P  A  G  D  A  G  P  G  D  R  T  P  A  E  T  L  L  C  E

16261 CTGCTGGCACGGGCCCTGGGCATCCCGGAGATCGACGCCGACGCCGACTTCCTGACGTCC 16320
      L  L  A  R  A  L  G  I  P  E  I  D  A  D  A  D  F  L  T  S

16321 GGCGGCACCAGCATCACCGCGCTGAAGCTGGTCGCCGGCGCCCGCCGGGTCGGCATCCGC 16380
      G  G  T  S  I  T  A  L  K  L  V  A  G  A  R  R  V  G  I  R

16381 CTCGAACTCACCACCGTCCTGCGCGAACGCACGGTGCGCCGCATCCTGGCGGCCCAGCCC 16440
      L  E  L  T  T  V  L  R  E  R  T  V  R  R  I  L  A  A  Q  P

16441 GACGCCGCCTCGCCCCTCGCCGAAGGAGTGCCCGAGTGACCGGTTCCGTAACGCTCACCC 16500
                                                M  T  G  S  V  T  L  T  P
      D  A  A  S  P  L  A  E  G  V  P  E  *   (orf39)

16501 CCCTCGGCGGGATCATCCCCAGGCCCCGCGGCGAGGGGCTCACCACCGGCGCCGAGTACG 16560
        L  G  G  I  I  P  R  P  R  G  E  G  L  T  T  G  A  E  Y  D

16561 ACCTGGGGCCGCTCGGCGACGCGGGCCCCGACTGgGTGCGGGCCCACGGCCCGCGACTGC 16620
        L  G  P  L  G  D  A  G  P  D  W  V  R  A  H  G  P  R  L  R

16621 GCGAGCGCCTCGCCACCGACGGGCTGATCCTGCTGCACGGTCTGCCCACCGACGGAGACG 16680
        E  R  L  A  T  D  G  L  I  L  L  H  G  L  P  T  D  G  D  G

16681 GCGTCGACGGCTTCCACGACGTCGTCGGCTCCGTCGGCGGCGACCCGCTGCCCTACACCG 16740
        V  D  G  F  H  D  V  V  G  S  V  G  G  D  P  L  P  Y  T  E

16741 AGCGCTCCACCCCGCGCAGCGTGGTCAAGGGCAACATCTACACCTCGACCGAGTACCCGG 16800
        R  S  T  P  R  S  V  V  K  G  N  I  Y  T  S  T  E  Y  P  A

16801 CCGACCAGCCCATCCCGATGCACAACGAGAACTCCTACGCCGCCCATTGGCCGTCCACGC 16860
        D  Q  P  I  P  M  H  N  E  N  S  Y  A  A  H  W  P  S  T  L

16861 TCTACTTCTTCTGCCACACCGCGCCGGACACCGGCGGGGCCACGCCGATCGCCGACGGCC 16920
        Y  F  F  C  H  T  A  P  D  T  G  G  A  T  P  I  A  D  G  R

16921 GCGCCGTCCTCGACCTCATCCCGGCCGAGGTCAGGCGGCGGTTCTCCCAAGGGGTCGTCT 16980
        A  V  L  D  L  I  P  A  E  V  R  R  R  F  S  Q  G  V  V  Y

16981 ACACCCGTACGTTCCGCGCCGACATGGGACTGAGCTGGCAGGAAGCGTTCCAGACCGAGG 17040
        T  R  T  F  R  A  D  M  G  L  S  W  Q  E  A  F  Q  T  E  D

17041 ACCGCGGCGACGTCGAACGCCATTGCCGCGCCCACGGCCAGGAGTTCTCCTGGGACGGCG 17100
        R  G  D  V  E  R  H  C  R  A  H  G  Q  E  F  S  W  D  G  D

17101 ACGTCCTGCGCACCCGCCACCACCGCCCGGCGACCGCCGTCGACCCCGGCACCGGAGCCG 17160
        V  L  R  T  R  H  H  R  P  A  T  A  V  D  P  G  T  G  A  E

17161 AGGTGTGGTTCAACCAGGCGCACCTGTTCCACCCGTCCAGCCTGGATCCCGACCTGCGCC 17220
        V  W  F  N  Q  A  H  L  F  H  P  S  S  L  D  P  D  L  R  Q

17221 AGGTGCTCCTGGAGACGTACGGCGAGAACGGCCTGCCCCGCGACGCCCTGTTCGCCGACG 17280
        V  L  L  E  T  Y  G  E  N  G  L  P  R  D  A  L  F  A  D  G

17281 GCACCCCGATCCCCGACGCCGACCTGGCAACGGTCCGCGCGGCCTACACCCGCGCCGCGC 17340
        T  P  I  P  D  A  D  L  A  T  V  R  A  A  Y  T  R  A  A  L
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17341  TCGCGCTGCCGTGGCGAGAGGGCGACATCATGCTGGTCGACAACCTGAGGATGGCCCACG   17400
         A  L  P  W  R  E  G  D  I  M  L  V  D  N  L  R  M  A  H  G

17401  GCCGCGAGCCCTTCACCGGCGAGCGCCGCGTACTCGTCGCGATGACCTCGGCGGACTCAT   17460
         R  E  P  F  T  G  E  R  R  V  L  V  A  M  T  S  A  D  S  *

17461  GAGCCGTGCCGACGCATCGGCACGCCGTCCTCCCGTCGGGGCGCTACCATCGCCGCTGTC   17520

17521  TCGGCCATCACCCCACCCGGGCGGAGGCAACCGGCCGTGCACATCCCCGCCGTGGTCGCC   17580

17581  ACGGCACGCGCGATCACCCGCGCCATGACCGCCCAGCCCGTTGTCACATCTGCGGAGGCG   17640

17641  CCGCGATGACAGAGGTCCGAGGTGAACTGATCCGGGCGCTGCCGGGTGTGCTGGAGGCGC   17700
           M  T  E  V  R  G  E  L  I  R  A  L  P  G  V  L  E  A  R
           (orf40)

17701  GTGCGGCGCGGGCGGGGCACACGACCGCCTTCCTCGACGCACGACGGTGTGTCACGTACC   17760
         A  A  R  A  G  H  T  T  A  F  L  D  A  R  R  C  V  T  Y  R

17761  GGGAGTTGGAGGCGCGCACCCGCCGGCTGGCGGGGTCACCTGGTGCGGTTGGGGGTGCGC   17820
         E  L  E  A  R  T  R  R  L  A  G  S  P  G  A  V  G  G  A  Q

17821  AGGGGCAGACCGGGTGGCGCTCGTCAATGGGCAACCGGGGTGGAGATGGCGGAGGGTTCC   17880
         G  Q  T  G  W  R  S  S  M  G  N  R  G  G  D  G  G  G  F  P

17881  CTCCCCGGTGCTGCGGGCCGGAGCGGTAGGGGTGCCGCTCGATTCCGGGGCCACGGACGC   17940
         P  R  C  C  G  P  E  R  *  G  C  R  S  I  P  G  P  R  T  R

17941  GGAGCTCGCGTACTTCCTCGACGACTGTGGAGCGGTGGCGGTGGTCACCGAGGAGACGCT   18000
         S  S  R  T  S  S  T  T  V  E  R  W  R  W  S  P  R  R  R  C

18001  GCTGCCGCGGGTCTCGCGATCGGCGGGCGTACGGATCCTGGTGGGGGGTTCGGACGCCGT   18060
         C  R  G  S  R  D  R  R  A  Y  G  S  W  W  G  V  R  T  P  S

18061  CCCGGAGGGAGCGGCTGCCGGCATCCACTCCTTCGAGCGGCTCGCGGCGTCGGATCCGGG   18120
         R  R  E  R  L  P  A  S  T  P  S  S  G  S  R  R  R  I  R  G

18121  GTGCGCGCCACGGGACGACCTCGGCCTCGACGAGCCGGCCTGGATCCTCTACACGTCGGG   18180
         A  R  H  G  T  T  S  A  S  T  S  R  P  G  S  S  T  R  R  G

18181  GACCACGGGCCGGAGCAAGGGCGTGGTCTGCGGCCAGCGCGCCGCGCTGTGGTCCGTGGC   18240
         P  R  A  G  A  R  A  W  S  A  A  S  A  P  R  C  G  P  W  R

18241  GGCGGCGTACGTGCCGTCGTGGGGTCTGGGGCCGCAGGACCGGCTGTTGTGGCCGCTGCC   18300
         R  R  T  C  R  R  G  V  W  G  R  R  T  G  C  C  G  R  C  P

18301  CATGTTCCACGCCTACGCGCACTCGCTGTGCCTGCTCGGGGTGGTGGCCGTGGGCGCGAG   18360
         C  S  T  P  T  R  T  R  C  A  C  S  G  W  W  P  W  A  R  A

18361  CGCGTACCTCCTCGACCGGGGCGCGAGCGTCGTCCGGGCGCTTGAGGAACAGCGGTGCAG   18420
         R  T  S  S  T  G  A  R  A  S  S  G  R  L  R  N  S  G  A  A

18421  CGTCGTGGCCGGTGTACCCGCCACCTACCGCCTGCTCACGAGCGCCTTCCGCGACGCCCC   18480
         S  W  P  V  Y  P  P  P  T  A  C  S  R  A  P  S  A  T  P  P

18481  CCGGCCACCGGCCGGCCTGCGACTGTGCGTCACCGGGGGCTGCGCCGTGCCCGCCGGGGC   18540
         G  H  R  P  A  C  D  C  A  S  P  G  A  A  P  C  P  P  G  L

18541  TGCGGGCGGACGTTGAGGAGCTGCTGGGCGTCCCGCTGCTCGACGGTTACGGCAGTACCG   18600
         R  A  D  V  E  E  L  L  G  V  P  L  L  D  G  Y  G  S  T  E
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18601  AGACCTGCGGCAAGATCACGGTTGAGCGGCTCGGCGGCTCCCGGGAGGGCGGTTGCCGGG   18660
         T  C  G  K  I  T  V  E  R  L  G  G  S  R  E  G  G  C  R
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SEQ ID NO: 3 BLM gene PPTase ORFS 41

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    1  GGATCCTGCGCTACCCGGACTTCGCCCAGTGGTGCGGCACCGAGCTCACCGCCGACTGGCACGTCCGCTTCCGGGCCGCC   80

   81  GCCGCGGTCTACGGGCATCTGCACATCCCCCGCGTGACCCGGTACGACGGCGTCCGCTTCGAGGAGGTGTCGGTCGGCTA  160

  161  CCCGCGCGAGTGGCGGCCCCGGCCGCCCCGCGAGCCGCTCCGGCAGATCCTGCCCCAGCCCGTCGACGAGCCGGGAGCCC  240

  241  TCTGGTGATCGCCGCCCTCCTGCCCTCCTGGGCCGTCACCGAACACGCCTTCACCGACGCCCCGGACGACCCGGTGAGCC  320
    1      M  I  A  A  L  L  P  S  W  A  V  T  E  H  A  F  T  D  A  P  D  D  P  V  S  L   26

  321  TCCTCTTCCCCGAGGAGGCCGCCCACGTCGCCCGCGCCGTCCCCAAGCGCCTGCACGAGTTCGCCACCGTCCGGGTGTGC  400
   27    L  F  P  E  E  A  A  H  V  A  R  A  V  P  K  R  L  H  E  F  A  T  V  R  V  C     52

  401  GCCCGCGCCGCCCTCGGCCGGCTGGGCCTCCCGCCCGGTCCGCTGCTGCCCGGCCGACGGGGCGCGCCGAGCTGGCCGGA  480
   53  A  R  A  A  L  G  R  L  G  L  P  P  G  P  L  L  P  G  R  R  G  A  P  S  W  P  D   79

  481  CGGGGTGGTGGGGAGCATGACGCACTGTCAGGGCTTCCGGGGCGCCGCGGTCGCCCGGGCCGCCGACGCCGCGTCGCTCG  560
   80   G  V  V  G  S  M  T  H  C  Q  G  F  R  G  A  A  V  A  R  A  A  D  A  A  S  L  G  106

  561  GGATAGACGCCGAGCCGAACGGGCCGCTCCCGGACGGCGTCCTCGCCATGGTCTCGCTGCCGTCCGAGCGCGAGTGGCTC  640
  107    I  D  A  E  P  N  G  P  L  P  D  G  V  L  A  M  V  S  L  P  S  E  R  E  W  L    132

  641  GCCGGACTGGCGGCCCGCCGGCCGGACGTGCACTGGGACCGGCTGCTGTTCAGCGCCAAGGAGAGCGTCTTCAAGGCGTG  720
  133  A  G  L  A  A  R  R  P  D  V  H  W  D  R  L  L  F  S  A  K  E  S  V  F  K  A  W   159

  721  GTACCCGCTGACCGGCCTGGAGCTGGACTTCGACGAGGCCGAGCTGGCCGTCGATCCGGACGCCGGGACGTTCACGGCCC  800
  160   Y  P  L  T  G  L  E  L  D  F  D  E  A  E  L  A  V  D  P  D  A  G  T  F  T  A  R   186

  801  GGCTGCTGGTGCCGGGACCGGTGGTCGGCGGCCGTCGGCTGGACGGGTTCGAGGGGCGCTGGGCGGCGGGCGAGGGCCTC  880
  187    L  L  V  P  G  P  V  V  G  G  R  R  L  D  G  F  E  G  R  W  A  A  G  E  G  L    212

  881  GTCGTCACGGCCATCGCCGTCGCGGCGCCGGCCGGTACCGCGGAGGAATCGGCGGAAGGGGCCGGGAAGGAAGCGACTGC  960
  213  V  V  T  A  I  A  V  A  A  P  A  G  T  A  E  E  S  A  E  G  A  G  K  E  A  T  A   239

  961  GGACGACCGGACCGCCGTCCCGTAAACCGCCCCGAACACCGGCGTGGCGCCCGCCGACCGTGTCGGGGGCGCCACGAACG  1040
  240   D  D  R  T  A  V  P  *                                                          247

 1041  GGCGCCGGCCCGGCGGGCCCTCCGCCGTGCGGAGCCGAGGCCCGGCGCGGACGCGCCCGGTGTCGTCGGATACGTGCGTC  1120

 1121  AGTCGGCGACGCAGACGTTGCCGTTGGTCGAGTTGAGCAGCCCGACGATGTCGATGGTGTTGCCGCAGAGGTTGATGGGG  1200

 1201  ATGTGGACGGGGATCTGGATGACGTTGCCCGAGACGACGCCCGGGGAGCCGACGGCCGCCCCCTTGGCGTTCGAGTCGGC  1280

 1281  GAGGGCGGTGCCGGAGACGCCGGCGAGCGCCGTGCCCACGGTGGCGGTGAGGGCCGCTGCCTTGGCGATTCGTGACATGG  1360

 1361  GGTGACACCTTCGTTCGGTCTGACAGGGTCGAGCTCACGGCCTCTGACGGCCGGGAGCCCGGATCAACGCCCGATCACCC  1440

 1441  CGAAGGTTTCGAATCGTGCGGCGGACGGGTGACCGGCGGCCGAACGGCCTCGCCGGGCCCCCGGAAGGTGCCATGACGTC  1520

 1521  CGTGCGCCATCTGTACAGCCCGGTCCCGCGCCGCGTACAAGGGACGGACGGACGGCCGGTGGACGGACGACCGGCGGGGA  1600

 1601  GGGGAGGCCATGAGCCGGATCGCGATCGTCGGGGCGGGTCAGGCCGGACTGCATCTGGCGCTGGGGCTGCTGGGGGCGGG  1680

 1681  GAGCGGCTCTTCCCGTCACGAGGTGCTGCTCGTGTCCGACGGGACGCCGGACGAGATCCGCGCCGGGCGGGTGCGGTCGA  1760

 1761  C  1761
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